

GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 13:10:59 ; Search time 29 Seconds
(without alignments)
227.362 Million cell updates/sec

Title: US-09-776-781-6
Perfect score: 158
Sequence: 1 MPTSSSTKTKTQLEHLLKLQMLNGINNY 32

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SPREMBL.21.*
- 2: sp_archaea.*
- 3: sp_bacteria.*
- 4: sp_fungi.*
- 5: sp_human.*
- 6: sp_invertebrate.*
- 7: sp_mammal.*
- 8: sp_mhc.*
- 9: sp_organelle.*
- 10: sp_phage.*
- 11: sp_plant.*
- 12: sp_rodent.*
- 13: sp_virus.*
- 14: sp_vertebrate.*
- 15: sp_unclassified.*
- 16: sp_rvirus.*
- 17: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	93.0	150	4 Q9C001	Q9C001 homo sapien
2	145	91.8	154	6 Q9XS38	Q9XS38 papio hamad
3	135.5	85.8	156	4 Q13169	Q13169 homo sapien
4	134	84.8	139	4 Q16334	Q16334 homo sapien
5	108.5	68.7	155	6 Q9XT83	Q9XT83 halichoerus
6	107.5	68.0	66	6 Q9BG74	Q9BG74 canis famil
7	107	67.7	79	6 Q9TV12	Q9TV12 canis famil
8	106	67.1	155	11 Q923T2	Q923T2 sigmodon hi
9	103	65.2	138	11 Q70329	Q70329 mesoicricetu
10	99	62.7	133	6 Q9WZR9	Q9WZR9 oryctolagus
11	84	53.2	23	4 Q9UCF5	Q9UCF5 homo sapien
12	78	49.4	154	6 Q9XT84	Q9XT84 delphinapte
13	75	47.5	152	11 Q88210	Q88210 cavia porce
14	72	45.6	69	6 Q9GJRA	Q9GJRA ovis aries
15	72	45.6	155	6 Q9GL83	Q9GL83 capra hircu
16	72	45.6	155	6 Q9SKP3	Q9SKP3 bubalus bub

17	69	43.7	39	6 Q9BG73	Q9BG73 canis famil
18	69	43.7	150	11 P70291	P70291 mus musculu
19	69	43.7	169	11 Q9QUS8	Q9QUS8 mus musculu
20	67	42.4	150	11 P70294	P70294 mus musculu
21	65.5	41.5	155	11 P70292	P70292 mus musculu
22	62.5	39.6	159	11 P70293	P70293 mus musculu
23	56	35.4	300	2 Q8VW37	Q8VW37 coxiellia bu
24	56	35.4	348	12 Q9DHS6	Q9DHS6 yaba-like d
25	53	33.5	251	12 Q9PYU2	Q9PYU2 xestia c-ni
26	53	33.5	452	10 Q9ZV75	Q9ZV75 arabidopsis
27	52	32.9	116	6 Q29138	Q29138 trichechus
28	52	32.9	478	17 Q8TLR6	Q8TLR6 methanosarc
29	51	32.3	517	16 Q8R6R8	Q8R6R8 thermoaner
30	51	32.3	737	16 Q9KTG5	Q9KTG5 vibrio chol
31	51	32.3	866	16 Q25517	Q25517 helicobacte
32	51	32.3	875	16 Q9ZK28	Q9ZK28 helicobacte
33	50	31.6	95	2 Q9F8U6	Q9F8U6 streptomyce
34	50	31.6	304	16 Q930K5	Q930K5 rhizobium m
35	50	31.6	543	16 Q9KSP8	Q9KSP8 vibrio chol
36	49.5	31.3	104	10 Q9FSQ4	Q9FSQ4 oryza sativ
37	49.5	31.3	367	10 Q9SIF5	Q9SIF5 arabidopsis
38	49.5	31.3	474	10 Q06376	Q06376 brassica na
39	49	31.0	145	16 Q9KAW0	Q9KAW0 bacillus ha
40	48.5	30.7	288	16 Q99TV7	Q99TV7 staphylococ
41	48.5	30.7	366	16 Q98G42	Q98G42 rhizobium l
42	48	30.4	311	16 Q9CLL6	Q9CLL6 pasteurella
43	48	30.4	398	16 Q50911	Q50911 borrelia bu
44	48	30.4	441	16 Q928V0	Q928V0 listeria in
45	48	30.4	441	16 Q69192	Q69192 listeria mo

ALIGNMENTS

RESULT 1

ID	Q9C001	PRELIMINARY;	PRT;	150 AA.
AC	Q9C001;			
DT	01-JUN-2001 (Tremblrel. 17, Created)			
DT	01-JUN-2001 (Tremblrel. 17, Last sequence update)			
DT	01-DEC-2001 (Tremblrel. 19, Last annotation update)			
DE	Interleukin-2 (Fragment).			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE-20545237; PubMed-11093171;			
RA	Matesanz F., Delgado C., Fresno M., Alcina A.;			
RT	"Allelic selection of human IL-2 gene."			
RL	Eur. J. Immunol. 30:3516-3521(2000).			
DR	EMBL; AF228636; AAG53575.1; -			
DR	HSSP; P01585; 3INK			
DR	InterPro; IPR000779; Interleukin-2.			
DR	Fram; PF00715; IL2; 1.			
DR	PRINTS; PD00265; INTERLEUKIN2.			
DR	ProDom; PD003649; Interleukin-2; 1.			
DR	SMART; SM00189; IL2; 1.			
DR	PROSITE; PS00424; INTERLEUKIN_2; 1.			
FT	NON_TER 150 150			
SQ	SEQUENCE 150 AA; 17312 MW; BF25860F8436ACE5 CRC64;			

Query Match 93.0%; Score 147; DB 4; Length 150;

Best Local Similarity 96.8%; Pred. No. 4.2e-14;

Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKTKTQLEHLLKLQMLNGINNY 32

Db 21 APTSSSTKTKTQLEHLLKLQMLNGINNY 51

RESULT 2

```
Q9XS38
ID Q9XS38 PRELIMINARY; PRT; 154 AA.
AC Q9XS38;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE IL-2.
OS Papio hamadryas (Hamadryas baboon),
OS Aotus lemurinus (Northern gray-necked night monkey),
OS Aotus nancymaae (Owl monkey),
OS Aotus nigriceps (black-headed night monkey), and
OS Aotus vociferans (noisy night monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Papio.
OX NCBI_TaxID=9557, 43147, 37293, 57175, 57176;
RN [1]
RP SEQUENCE FROM N.A.
RA Murillo L.A., Hernandez E., Echeverry S.J., Mendez J.A., Moreno A.,
RA Patarroyo M.E.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88365; AAD41538.1; -
DR EMBL; U88364; AAD41534.1; -
DR EMBL; U88361; AAD41535.1; -
DR EMBL; U88363; AAD41536.1; -
DR EMBL; U88362; AAD41537.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17675; AB752ABBADA96469 CRC64;

Query Match 91.8%; Score 145; DB 6; Length 154;
Best Local Similarity 93.5%; Pred. No. 8.5e-14;
Matches 29; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKTKTQLEHLLKQMLNGINNY 32
| | | | | | | | | | | | | | | | | | | | | |
Db 21 APTSSSTKTKTQLEHLLDQLMLNGINNY 51
| | | | | | | | | | | | | | | | | | | | | |

RESULT 3
Q13169
ID Q13169 PRELIMINARY; PRT; 156 AA.
AC Q13169;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interleukin 2.
GN IL2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu D., Wu Y., Chen J., Yu L., Zhong M., Hui Y., Qu H.;
RA "Expression of human IL-2 from gene transferred mouse melanoma cells
RT and its effect on the growth of mouse melanoma.";
RL Chung-Hua Min Kuo Wei Sheng Wu Chi Mien I Hsueh Tsa Chih
RL 13:78-82(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Xu L.;
RA Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.
RL EMBL; U25676; AAA70092.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.

us-09-776-781-6.rspt
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 156 AA; 18002 MW; 8E0452D43B336389 CRC64;

Query Match 85.8%; Score 135.5; DB 4; Length 156;
Best Local Similarity 88.2%; Pred. No. 2.3e-12;
Matches 30; Conservative 0; Mismatches 1; Indels 3; Gaps 1;

QY 2 APTSSS---TKKTQLEHLLKQMLNGINNY 32
| | | | | | | | | | | | | | | | | | | | | |
Db 21 APTSSSTKTKTQLEHLLDQLMLNGINNY 54
| | | | | | | | | | | | | | | | | | | | | |

RESULT 4
Q16334
ID Q16334 PRELIMINARY; PRT; 139 AA.
AC Q16334;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2001 (TrEMBLrel. 18, Last annotation update)
DE IL-2 protein (Fragment).
GN IL-2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95239150; PubMed=7722480;
RA Eisenberg O., Faber-Elman A., Lotan M., Schwartz M.;
RA "Interleukin-2 transcripts in human and rodent brains: possible
RT expression by astrocytes.";
RL J. Neurochem. 64:1928-1936(1995).
DR EMBL; S77835; AAD14264.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 139 AA; 15986 MW; 731FBA406D0C63C5 CRC64;

Query Match 84.8%; Score 134; DB 4; Length 139;
Best Local Similarity 90.3%; Pred. No. 3.4e-12;
Matches 28; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 APTSSSTKTKTQLEHLLKQMLNGINNY 32
| | | | | | | | | | | | | | | | | | | | | |
Db 17 APTSSSTKTKTQLEHLLDQLMLNGINNY 47
| | | | | | | | | | | | | | | | | | | | | |

RESULT 5
Q9XT83
ID Q9XT83 PRELIMINARY; PRT; 155 AA.
AC Q9XT83;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Interleukin 2.
OS Halichoerus grypus (Gray seal).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Halichoerus.
OX NCBI_TaxID=9711;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99221046; PubMed=10206205;
RA St-Laurent G., Beliveau C., Archambault D.;
RA "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) Interleukin
RT 2.";
```



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RC TISSUE=SPLEEN;
RX MEDLINE=98234044; PubMed=95731100;
RA Melby P.C., Tryon V.V., Chandrasekar B., Freeman G.L.;
RT "Cloning of Syrian hamster (Mesocricetus auratus) cytokine cDNAs and
RT analysis of cytokine mRNA expression in experimental visceral
RT leishmaniasis.";
RL Infect. Immun. 66:2135-2142(1998).
DR EMBL; AF046212; AAC40097.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
FT NON_TER 1
FT NON_TER 138
SQ SEQUENCE 138 AA; 15739 MW; 351032995B670779 CRC64;

Query Match 65.2%; Score 103; DB 11; Length 138;
Best Local Similarity 71.0%; Pred. No. 1.4e-07;
Matches 22; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKTQLEHLLKQLMILNGINNY 32
Db 14 APTSSSKKETQHQLEQLLDLQLKLGINNY 44

RESULT 10
Q9M2R9 PRELIMINARY; PRT; 133 AA.
AC Q9M2R9;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Interleukin 2 variant IL2delta2.
GN IL-2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=5986;
RN [1]
SEQUENCE FROM N.A.
RC TISSUE=SPLEEN, AND LYMPH NODE;
RX MEDLINE=20304114; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
RT "The complete cDNA sequences of IL-2, IL-4, IL-6 and IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytokine 12:553-565(2000).
DR EMBL; AF169168; AAF86652.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 133 AA; 14748 MW; 0D54758C190B5655 CRC64;

Query Match 62.7%; Score 99; DB 6; Length 133;
Best Local Similarity 69.0%; Pred. No. 5.5e-07;
Matches 20; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 APTSSSTKTQLEHLLKQLMILNGIN 30
Db 21 APTSSSKETQEQDQLLDLQLVLLKGVN 49

RESULT 11
Q9UCF5 PRELIMINARY; PRT; 23 AA.
ID Q9UCF5
AC Q9UCF5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
OS Cavia porcellus (Guinea pig).
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DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE Interleukin 2 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
SEQUENCE.
RX MEDLINE=93289963; PubMed=8512072;
RA Mullner S., Karbe-Thonges B., Tripler D.;
RT "Charge heterogeneity of insulin fusion proteins expressed in
RT Escherichia coli is not due to proteolytic degradation.";
RL Anal. Biochem. 210:366-373(1993).
SQ SEQUENCE 23 AA; 2637 MW; 40B64C6875CE021F CRC64;

Query Match 53.2%; Score 84; DB 4; Length 23;
Best Local Similarity 85.7%; Pred. No. 1.7e-05;
Matches 18; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 TSSTKTKTQLEHLLKQLM 24
Db 3 TSXSTKTKTQLEHLLKQLM 23

RESULT 12
Q9XT84 PRELIMINARY; PRT; 154 AA.
ID Q9XT84;
AC Q9XT84;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Interleukin 2.
OS Delphinapterus leucas (Beluga whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti;
OC Monodontidae; Delphinapterus.
OX NCBI_TaxID=9749;
RN [1]
SEQUENCE FROM N.A.
RX MEDLINE=99221046; PubMed=10206205;
RA St-Laurent G., Bellevue C., Archambault D.;
RT "Molecular cloning and phylogenetic analysis of beluga whale
RT (Delphinapterus leucas) and grey seal (Halichoerus grypus) Interleukin
RT 2.";
RL Vet. Immunol. Immunopathol. 67:385-394(1999).
DR EMBL; AF072870; AAD40847.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 154 AA; 17652 MW; 4288D3D41D04F172 CRC64;

Query Match 49.4%; Score 78; DB 6; Length 154;
Best Local Similarity 51.6%; Pred. No. 0.00088;
Matches 16; Conservative 7; Mismatches 8; Indels 0; Gaps 0;

QY 2 APTSSSTKTQLEHLLKQLMILNGINNY 32
Db 21 APTSSSTENTKQVQLQLDLHLLKLEINNH 51

RESULT 13
O88210 PRELIMINARY; PRT; 152 AA.
ID O88210;
AC O88210;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-OCT-2001 (TReMBLrel. 18, Last annotation update)
DE Interleukin 2 precursor.
OS Cavia porcellus (Guinea pig).
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RESULT 15
Q9GL83 ID Q9GL83 PRELIMINARY; PRT; 155 AA.
AC Q9GL83;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 15, Last annotation update)
DE Interleukin 2.
GN IL-2.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OC NCBI_TaxID=9925;
DE NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RA Ying Q.H., Li X.R., Pan J.Y.;
RT "Cloning of the goat IL-2 gene and its expression in E.coli.";
RL Submitted (SEP-2000) to the EMBL/GenBank/DDJB databases.
DR EMBL; AF307018; AAG28783.1; -
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
SQ SEQUENCE 155 AA; 17605 MW; EEE82DE18F5469AA CRC64;

Query Match 45.68; Score 72; DB 6; Length 155;
Best Local Similarity 50.08; Pred. No. 0.007;
Matches 15; Conservative 6; Mismatches 9; Indels 0;

QY 2 APTSSSTKKTQLQLHLLKLQMLINGIN 31
||||||| |:: ||| ||::|
DB 21 APTSSSTGNTMKVKVSLDLLQLLLGKVN 50

Search completed: November 22, 2002, 13:13:05
Job time : 31 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 13:09:49 ; Search time 10 Seconds
(without alignments)
132.724 Million cell updates/sec

Title: US-09-776-781-6

Perfect score: 158

Sequence: 1 MAPTSSSTKTKTQLEHLLKLQMLINGINNY 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	147	93.0	153	1 IL2_HUMAN	P01585 homo sapien
2	147	93.0	154	1 IL2_MACFA	Q29615 macaca fasc
3	147	93.0	154	1 IL2_MACMU	P51498 macaca mula
4	142	89.9	154	1 IL2_CERTO	P46649 cercocobus
5	116	73.4	154	1 IL2_MIRAN	O62641 mirounga an
6	107.5	68.0	155	1 IL2_CANFA	Q29416 canis famil
7	107	67.7	153	1 IL2_RABIT	O77620 oryctolaqus
8	107	67.7	154	1 IL2_FELCA	Q07885 felis silve
9	97	61.4	155	1 IL2_RAT	P17108 rattus norv
10	96	60.8	154	1 IL2_PIG	P26891 sus scrofa
11	95	60.1	155	1 IL2_MERUN	Q08081 meriones un
12	88	55.7	152	1 IL2_ORCOR	O97513 orcinus orc
13	85	53.8	149	1 IL2_HORSE	P37997 equus cabal
14	72	45.6	155	1 IL2_BOVIN	P05016 bos taurus
15	72	45.6	155	1 IL2_CAPHI	P36835 capra hircu
16	72	45.6	155	1 IL2_SHEEP	P19114 ovis aries
17	72	45.6	162	1 IL2_CEREL	P51747 cervus elap
18	64.5	40.8	166	1 IL2_MUSSP	Q08867 mus spretus
19	64	40.5	169	1 IL2_MOUSE	P04351 mus musculu
20	61	38.6	189	1 Y064_METJA	Q60376 methanococc
21	56	35.4	1046	1 POL_SIVAG	P27980 simian immu
22	54	34.2	1061	1 POL_SIVAT	P05895 simian immu
23	53	33.5	357	1 AAAA_EMENI	P21133 emericella
24	51.5	32.6	415	1 CGA2_XENLA	P47827 xenopus lae
25	51	32.3	746	1 PCAP_HUMAN	Q96rn5 homo sapien
26	51	32.3	792	1 PCAP_MOUSE	Q924h2 mus musculu
27	50.5	32.0	741	1 RN5A_HUMAN	Q05823 homo sapien
28	48.5	30.7	452	1 TRFC_HELPY	O25867 helicobacte
29	47.5	30.1	150	1 RNK6_SAISS	O46529 salmirci sci
30	47.5	30.1	154	1 RNK6_BOVIN	P08904 bos taurus
31	47	29.7	257	1 ABCX_GALSU	P35020 galdieria s
32	47	29.7	406	1 CGA2_BOVIN	P30274 bos taurus
33	47	29.7	421	1 CGA1_MOUSE	Q61456 mus musculu

ALIGNMENTS

RESULT 1

ID	IL2_HUMAN	STANDARD	PRT	153 AA
AC	P01585;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUN-2002 (Rel. 41, Last annotation update)			
DE	Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)			
DE	(Aldesleukin).			
GN	IL2.			
OS	Homo sapiens (Human), and			
OS	Hylobates lar (Common gibbon).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606, 9580;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=84247353; PubMed=6330695;			
RA	Holbrook N.J., Lieber M., Crabtree G.R.;			
RT	"DNA sequence of the 5' flanking region of the human interleukin 2			
RT	gene: homologies with adult T-cell leukemia virus.;"			
RL	Nucleic Acids Res. 12:5005-5013(1984).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=83167472; PubMed=6403867;			
RA	Taniguchi T., Matsui H., Fujita T., Takaoka C., Kashima N.,			
RA	Yoshimoto R., Hamuro J.;			
RT	"Structure and expression of a cloned cDNA for human interleukin-2.;"			
RL	Nature 302:305-310(1983).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=84023840; PubMed=6312994;			
RA	Maeda S., Nishino N., Obaru K., Mita S., Nomiyama H., Shimada K.,			
RA	Fujimoto K., Teranishi T., Hirano T., Onoue K.;			
RT	"Cloning of interleukin 2 mRNAs from human tonsils.;"			
RL	Biochem. Biophys. Res. Commun. 115:1040-1047(1983).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=83246551; PubMed=6306584;			
RA	Devos R., Plaetinck G., Cheroutre H., Simons G., Degraeve W.,			
RA	Tavernier J., Remaut E., Fiers W.;			
RT	"Molecular cloning of human interleukin 2 cDNA and its expression in			
RT	E. coli.;"			
RL	Nucleic Acids Res. 11:4307-4323(1983).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RC	SPECIES=Human;			
RX	MEDLINE=84170356; PubMed=6608729;			
RA	Holbrook N.J., Smith K.A., Fornace A.J. Jr., Comeau C.M.,			
RA	Wiskocil R.L., Crabtree G.R.;			
RT	"T-cell growth factor: complete nucleotide sequence and organization			
RT	of the gene in normal and malignant cells.;"			

34	47	29.7	432	1	CGA2_HUMAN	P20248 homo sapien
35	47	29.7	465	1	CGA1_HUMAN	P78396 homo sapien
36	47	29.7	943	1	YLM5_CAEEL	P34408 caenorhabdi
37	47	29.7	1492	1	CFTR_SOUAC	P26362 squalus aca
38	46.5	29.4	989	1	T100_HUMAN	O75448 homo sapien
39	46	29.1	532	1	G6PI_BORBU	O51672 borrelia bu
40	46	29.1	1403	1	PRO_DRONE	P29617 drosophila
41	45	28.5	81	1	EX7S_PASMD	Q9cna0 pasteurella
42	45	28.5	155	1	YHCH_HAEIN	P44433 haemophilus
43	45	28.5	351	1	YNX1_YEAST	P53860 saccharomyc
44	45	28.5	368	1	LEU3_NEUCR	P34738 neurospora
45	45	28.5	479	1	ZW10_DROPS	O44218 drosophila

RL PROC. Natl. Acad. Sci. U.S.A. 81:1634-1638(1984).
 RP [6]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Human;
 RX MEDLINE=84170243; PubMed=6324170;
 RA Fujita T., Takaoaka C., Matsui H., Taniguchi T.;
 RT "Structure of the human interleukin 2 gene.";
 RL Proc. Natl. Acad. Sci. U.S.A. 80:7437-7441(1983).
 RN [7]
 RN SEQUENCE FROM N.A.
 RP SPECIES=Human;
 RX MEDLINE=95239150; PubMed=7722480;
 RA Eizenberg O., Faber-Elman A., Iotani M., Schwartz M.;
 RT "Interleukin-2 transcripts in human and rodent brains: possible
 expression by astrocytes.";
 RL J. Neurochem. 64:1928-1936(1995).
 RN [8]
 RN SEQUENCE FROM N.A.
 RP SPECIES=Human;
 RX MEDLINE=96422299; PubMed=8824916;
 RA Chernicky C.L., Tan H., Burfeind P., Ilan J., Ilan J.;
 RT "Sequence of Interleukin-2 isolated from human placental poly A+ RNA:
 possible role in maintenance of fetal allograft.";
 RL Mol. Reprod. Dev. 43:180-186(1996).
 RN [9]
 RN SEQUENCE FROM N.A.
 RP SPECIES=Human;
 RX MEDLINE=87064618; PubMed=3491296;
 RA Siebenlist U., Durand D.B., Bressler P., Holbrook N.J., Norris C.A.,
 RA Ramoun M., Kant J.A., Crabtree G.R.;
 RT "Promoter region of interleukin-2 gene undergoes chromatin structure
 changes and confers inducibility on chloramphenicol acetyltransferase
 gene during activation of T cells.";
 RL Mol. Cell. Biol. 6:3042-3049(1986).
 RN [12]
 RN SEQUENCE OF 1-68 FROM N.A.
 RP SPECIES=Human;
 RX MEDLINE=85038540; PubMed=6333684;
 RA Robb R.J., Kutny R.M., Penico M., Morris H.R., Chowdhry V.;
 RT "Amino acid sequence and post-translational modification of human
 interleukin 2.";
 RL Proc. Natl. Acad. Sci. U.S.A. 81:6486-6490(1984).
 RN [14]
 RN CARBOHYDRATE-LINKAGE SITE.
 RP SPECIES=Human;
 RX MEDLINE=90008901; PubMed=2793860;
 RA Conradt H.S., Nimcz M., Dittmar K.E.J., Lindenmaier W., Hoppe J.,
 RA Hauser H.;
 RT "Expression of human interleukin-2 in recombinant baby hamster
 kidney, Ltk-, and Chinese hamster ovary cells. Structure of O-linked
 carbohydrate chains and their location within the polypeptide.";
 *RL J. Biol. Chem. 264:17368-17373(1989).

RN SEQUENCE FROM N.A.
 RP SPECIES=Human;
 RX MEDLINE=88070646; PubMed=3500515;
 RA Brandhuber B.J., Boone T., Kenney W.C., McKay D.B.;
 RT "Three-dimensional structure of interleukin-2.";
 RL Science 238:1707-1709(1987).
 RN [17]
 RN X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS).
 RP SPECIES=Human;
 RX MEDLINE=92335891; PubMed=1631562;
 RA Bazan J.F.;
 RT "Unraveling the structure of IL-2.";
 RL Science 257:410-412(1992).
 RN [18]
 RN RESPONSE TO ABOVE LETTER.
 RA McKay D.B.;
 RL Science 257:412-413(1992).
 RN [19]
 RN STRUCTURE BY NMR.
 RP MEDLINE=92379010; PubMed=1510960;
 RA Mott H.R., Driscoll P.C., Boyd J., Cooke R.M., Weir M.P.,
 RA Campbell I.D.;
 RT "Secondary structure of human interleukin 2 from 3D heteronuclear NMR
 experiments.";
 RL Biochemistry 31:7741-7744(1992).
 RN [20]
 RN 3D-STRUCTURE MODELING.
 RX MEDLINE=95111955; PubMed=7529123;
 RA Bamorough P., Hedgecock C.J., Richards W.G.;
 RT "The interleukin-2 and interleukin-4 receptors studied by molecular
 modelling.";
 RL Structure 2:839-851(1994).
 CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
 CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
 CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
 CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
 CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- DISEASE: A FORM OF T-CELL ACUTE LYMPHOBLASTIC LEUKEMIA (T-ALL) IS
 CC CHARACTERIZED BY A CHROMOSOMAL TRANSLOCATION T(4;16)(Q26;P13)
 CC WHICH INVOLVES IL2 AND BCMA.
 CC -!- PHARMACEUTICAL: Available under the name Proleukin (Chiron). Used
 CC in patients with renal cell carcinoma or metastatic melanoma.
 CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
 CC -!- DATABASE: NAME-RED Systems' cytokine source book: IL2;
 CC WWW="http://www.fndsystems.com/asp/g-sitebuilder.asp?bodyId=206".
 CC -----
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 DR EMBL: J00264; A048509.1; -
 DR EMBL: X01586; CA25742.1; -
 DR EMBL: V00564; CA23827.1; -
 DR EMBL: X00695; CA25252.1; -
 DR EMBL: K02056; AAA98792.1; -
 DR EMBL: M13879; AAA59141.1; -
 DR EMBL: K03174; AAA35453.1; -
 DR EMBL: S77834; A014263.2; -
 DR EMBL: S62692; A046883.1; -


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Query Match          93.0%; Score 147; DB 1; Length 153;
Best Local Similarity 96.8%; Pred. No. 5.8e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLINGINNY 32
DB 21 APTSSSTKKTQLEHLLKLQMLINGINNY 51

RESULT 2
IL2_MACFA
ID IL2_MACFA STANDARD; PRT; 154 AA.
AC Q29615;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9541;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Peripheral blood;
RA Yabe M., Matsuura Y., Tatsumi M.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC
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CC
CC EMBL; D63352; BAA09676.1; -.
CC HSP; P01585; 3INK.
CC InterPro: IPR000779; Interleukin-2.
CC Pfam: PF00715; IL2; 1.
CC PRINTS; PR00285; INTERLEUKIN2.
CC ProDom; PD003649; Interleukin-2; 1.
CC SMART; SM00189; IL2; 1.
CC PROSITE; PS00424; INTERLEUKIN2; 1.
CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
CC T-cell.
CC SIGNAL 1 20 BY SIMILARITY.
CC CHAIN 21 154 INTERLEUKIN-2.
CC CARBOHYD 23 23 O-LINKED (GALNAc. . .) (BY SIMILARITY).
CC DISULFID 78 126 BY SIMILARITY.
CC SEQUENCE 154 AA; 17686 MW; 7853FE624A5E4A49 CRC64;

Query Match          93.0%; Score 147; DB 1; Length 154;
Best Local Similarity 96.8%; Pred. No. 5.8e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLINGINNY 32
DB 21 APTSSSTKKTQLEHLLKLQMLINGINNY 51

RESULT 3
IL2_MACMU
ID IL2_MACMU STANDARD; PRT; 154 AA.
AC P51498;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Macaca mulatta (Rhesus macaque), and
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9544, 9545;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Villinger F.J., Brar S.S., Mayne A.E., Chikkala N., Ansari A.A.;
RL MEDLINE=96003435; PubMed=7561102;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates."
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC
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CC
CC EMBL; U19847; AAB60400.1; -.
CC EMBL; U19852; AAA86714.1; -.
CC HSP; P01585; 3INK.
CC InterPro: IPR000779; Interleukin-2.
CC Pfam: PF00715; IL2; 1.
CC PRINTS; PR00285; INTERLEUKIN2.
CC ProDom; PD003649; Interleukin-2; 1.
CC SMART; SM00189; IL2; 1.
CC PROSITE; PS00424; INTERLEUKIN2; 1.
CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
CC T-cell.
CC SIGNAL 1 20 BY SIMILARITY.
CC CHAIN 21 154 INTERLEUKIN-2.
CC CARBOHYD 23 23 O-LINKED (GALNAc. . .) (BY SIMILARITY).
CC DISULFID 78 126 BY SIMILARITY.
CC SEQUENCE 154 AA; 17685 MW; 6AEB480F204BA49 CRC64;

Query Match          93.0%; Score 147; DB 1; Length 154;
Best Local Similarity 96.8%; Pred. No. 5.8e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLINGINNY 32
DB 21 APTSSSTKKTQLEHLLKLQMLINGINNY 51

RESULT 4
IL2_CERTO
ID IL2_CERTO STANDARD; PRT; 154 AA.
AC P46649;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.

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```

OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA MEDLINE=96003435; PubMed=7561102;
RX Villinger F.J., Brar S.S., Wayne A.E., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and
RT nonhuman primates";
RL J. Immunol. 155:3946-3954(1995).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC
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CC
CC EMBL; U19846; AAB50399.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
FT VARIANT 25 25 R -> S.
FT VARIANT 74 74 K -> E.
SQ SEQUENCE 154 AA; 17754 MW; 9FEB51814204BA48 CRC64;

Query Match 89.9%; Score 142; DB 1; Length 154;
Best Local Similarity 93.5%; Pred. No. 3.3e-14;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLMILNGINNY 32
Db 21 APTSRSTKKTQLEHLLKQLMILNGINNY 51
|||||
RESULT 5
IL2_MIRAN STANDARD; PRT; 154 AA.
AC O62641;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Mirounga angustirostris (Northern elephant seal).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Mirounga.
OX NCBI_TaxID=9716;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98136706; PubMed=9476229;
RA Shoda L.K.M., Brown W.C., Rice-Ficht A.C.;

Query Match 89.9%; Score 142; DB 1; Length 154;
Best Local Similarity 93.5%; Pred. No. 3.3e-14;
Matches 29; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLMILNGINNY 32
Db 21 APTSRSTKKTQLEHLLKQLMILNGINNY 51
|||||
RESULT 5
IL2_MIRAN STANDARD; PRT; 154 AA.
AC O62641;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Mirounga angustirostris (Northern elephant seal).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Pinnipedia; Phocidae; Mirounga.
OX NCBI_TaxID=9716;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98136706; PubMed=9476229;
RA Shoda L.K.M., Brown W.C., Rice-Ficht A.C.;

```

```

RT "Sequence and characterization of phocine interleukin 2.";
RL J. Wildl. Dis. 34:81-90(1998).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION. THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC
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CC
CC EMBL; U79187; AAC12258.1; -.
DR HSSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 154 INTERLEUKIN-2.
FT CARBOHYD 23 23 O-LINKED (GALNAC. . .) (BY SIMILARITY).
FT DISULFID 78 126 BY SIMILARITY.
FT SEQUENCE 154 AA; 17661 MW; 0C92337A4B16B6BB CRC64;

Query Match 73.4%; Score 116; DB 1; Length 154;
Best Local Similarity 71.0%; Pred. No. 2.6e-10;
Matches 22; Conservative 6; Mismatches 3; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLMILNGINNY 32
Db 21 APTSSSTKKTQLEHLLKQLMILNGINNY 51
|||||
RESULT 6
IL2_CANFA STANDARD; PRT; 155 AA.
ID IL2_CANFA
AC Q29416; Q28249;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=XBRED21/12/93; TISSUE=Lymph node;
RX MEDLINE=95337423; PubMed=7612930;
RA Dunham S.P., Argyle D.J., Onions D.E.;
RT "The isolation and sequence of canine interleukin-2.";
RL DNA Seq. 5:177-180(1995).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=96016696; PubMed=8571541;
RA Somberg R.L., Pullen R.P., Casal M.L., Patterson D.F., Felsburg P.J.,
RA Henthorn P.S.;
RT "A single nucleotide insertion in the canine interleukin-2 receptor
RT gamma chain results in X-linked severe combined immunodeficiency
RT disease.";
RL Vet. Immunol. Immunopathol. 47:203-213(1995).

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[3]
SEQUENCE FROM N.A.
STRAIN=Beagle; Tissue=Spleen;
MEDLINE=95347614; PubMed=7622066;
RA Knapp D.W., Williams J.S., Andrisani O.M.;
RT "Cloning of the canine interleukin-2 encoding cDNA.";
RL Gene 159:281-282(1995).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
CC
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CC
CC EMBL: D30710; BAA06378.1; -
CC EMBL: U28141; AAB68969.1; -
CC EMBL: U11689; AAB75360.1; -
CC HSP: P01585; 3INK.
CC InterPro: IPR000779; Interleukin-2.
CC Pfam: PF00715; IL2; 1.
CC PRINTS: PR00265; INTERLEUKIN2.
CC ProDom: PD003649; Interleukin-2; 1.
CC SMART: SM00189; IL2; 1.
CC PROSITE: PS00424; INTERLEUKIN_2; 1.
CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
CC T-cell.
CC SIGNAL 1 20 BY SIMILARITY.
CC CHAIN 21 155 INTERLEUKIN-2.
CC CARBOHYD 24 24 O-LINKED (GLNAC. . .) (BY SIMILARITY).
CC FT CARBOHYD 112 112 N-LINKED (GLNAC. . .) (POTENTIAL).
CC FT DISULFID 79 127 BY SIMILARITY.
CC FT CONFLICT 4 4 M -> I (IN REF. 3).
CC FT CONFLICT 37 37 Q -> R (IN REF. 3).
CC FT CONFLICT 151 151 F -> Y (IN REF. 3).
CC FT CONFLICT 154 154 L -> M (IN REF. 3).
CC SEQUENCE 155 AA; 17668 MW; D123E486B7F4AC1D CRC64;

Query Match 68.0%; Score 107.5; DB 1; Length 155;
Best Local Similarity 68.8%; Pred. No. 4.9e-09;
Matches 22; Conservative 6; Mismatches 3; Indels 1; Gaps 1;

OY 2 AP-TSSSTKTKTQLQLEHLLKQLMILNGINNY 32
|| |||||:|:|:| |||||:|:|:|
Db 21 APITSSSTKETEQQLDQLLLQLLNGVNNY 52

RESULT 7
IL2_RABIT
ID IL2_RABIT STANDARD; PRT; 153 AA.
AC Q77620;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lymph node;
RA MEDLINE=20304414; PubMed=10843729;
RA Perkins H.D., van Leeuwen B.H., Hardy C.M., Kerr P.J.;
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RT "The complete cDNA sequences of IL-2, IL-4, IL-6 AND IL-10 from the
RT European rabbit (Oryctolagus cuniculus).";
RL Cytokine 12:555-565(2000).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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CC
CC EMBL: AF068057; AAC23838.1; -
CC HSP: P01585; 3INK.
CC InterPro: IPR000779; Interleukin-2.
CC Pfam: PF00715; IL2; 1.
CC PRINTS: PR00265; INTERLEUKIN2.
CC ProDom: PD003649; Interleukin-2; 1.
CC SMART: SM00189; IL2; 1.
CC PROSITE: PS00424; INTERLEUKIN_2; 1.
CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
CC T-cell.
CC SIGNAL 1 20 BY SIMILARITY.
CC CHAIN 21 153 INTERLEUKIN-2.
CC CARBOHYD 23 23 O-LINKED (GLNAC. . .) (BY SIMILARITY).
CC FT CARBOHYD 111 111 N-LINKED (GLNAC. . .) (POTENTIAL).
CC FT DISULFID 78 125 BY SIMILARITY.
CC SEQUENCE 153 AA; 17256 MW; 8173536B2DD8B86 CRC64;

Query Match 67.7%; Score 107; DB 1; Length 153;
Best Local Similarity 67.7%; Pred. No. 5.8e-09;
Matches 21; Conservative 6; Mismatches 4; Indels 0; Gaps 0;

OY 2 APTSSSTKTKTQLQLEHLLKQLMILNGINNY 32
|| |||||:|:|:| |||||:|:|:|
Db 21 APTSSSTKTKTQLDQLLLQLLNGVNDY 51

RESULT 8
IL2_FELCA
ID IL2_FELCA STANDARD; PRT; 154 AA.
AC Q07885;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93356765; PubMed=8352761;
RA Cozzi P.J., Padrid P.A., Takeda J., Alegre M.-A., Yuhki N.,
RA Leff A.R.;
RT "Sequence and functional characterization of feline interleukin 2.";
RL Biochem. Biophys. Res. Commun. 194:1038-1043(1993).
RN [2]
RP SEQUENCE FROM N.A.
RA Litman R., Gibbs C., Good R.A., Day N.K.;
RA Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
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CC EMBL; X56750; CAA40071.1; -
CC EMBL; X58428; CAA41330.1; -
CC EMBL; AB041935; BAB16110.1; -
CC PIR; S15473; S15473.
CC PIR; S16241; S16241.
CC HSP; P01585; 3INK.
CC InterPro; IPR000779; Interleukin-2.
CC Pfam; PF00715; IL2; 1.
CC PRINTS; PR00265; INTERLEUKIN2.
CC ProDom; PD003649; Interleukin-2; 1.
CC SMART; SM00189; IL2; 1.
CC PROSITE; PS00424; INTERLEUKIN_2; 1.
CC Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
CC T-cell.
CC SIGNAL 1 20 BY SIMILARITY.
CC CHAIN 21 154 INTERLEUKIN-2.
CC CARBOHYD 23 23 O-LINKED (GALNAc. . .) (BY SIMILARITY).
CC DISULFID 78 126 BY SIMILARITY.
CC SEQUENCE 154 AA; 17401 MW; F3B95E43D4A3D3E1 CRC64;

Query Match 60.8%; Score 96; DB 1; Length 154;
Best Local Similarity 64.5%; Pred. No. 2.6e-07;
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

OY 2 APTSSSTKTKTQLEHLLKLMILNGINNY 32
||||| 1: | | | | | 1: | | | | |
DB 21 APTSSSTKTKKQLEPLDLLDQLLLKEVKNY 51

RESULT 11
IL2_MERUN STANDARD; PRT; 155 AA.
ID IL2_MERUN
AC Q08081;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Meriones unguiculatus (Mongolian jird) (Mongolian gerbil).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Gerbillinae;
OC Meriones.
OX NCBI_TaxID=10047;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=94174702; PubMed=8128610;
RA Mai Z., Kousoulas K.G., Horohov D.W., Klei T.R.;
RT "Cross-species PCR cloning of gerbil (Meriones unguiculatus)
interleukin-2 cDNA and its expression in COS-7 cells.";
RL Vet. Immunol. Immunopathol. 40:63-71(1994).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.

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CC EMBL; X68779; CAA48679.1; -

DR PIR; S33509; S33509.
DR HSP; P01585; 3INK.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
DR T-cell.
DR SIGNAL 1 20 BY SIMILARITY.
DR CHAIN 21 155 INTERLEUKIN-2.
DR CARBOHYD 23 23 O-LINKED (GALNAc. . .) (BY SIMILARITY).
DR DISULFID 78 126 BY SIMILARITY.
DR SEQUENCE 155 AA; 17602 MW; DOF74AA1A381CDDA CRC64;

Query Match 60.1%; Score 95; DB 1; Length 155;
Best Local Similarity 64.5%; Pred. No. 3.7e-07;
Matches 20; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

OY 2 APTSSSTKTKTQLEHLLKLMILNGINNY 32
||||| 1: | | | | | 1: | | | | |
DB 21 APTSSPAKEAQVLEQLLLDQLLLRGINNY 51

RESULT 12
IL2_ORCOR STANDARD; PRT; 152 AA.
ID IL2_ORCOR
AC O97513;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF)
DE (Fragment).
GN IL2.
OS Orcinus orca (Killer whale).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Cetacea; Odontoceti; Delphinidae;
OC Orcinus.
OX NCBI_TaxID=9733;
RN [1]
RP SEQUENCE FROM N.A.
RA Ness T.L., Bradley W.G., Reynolds J.E. III, Roess W.B.;
RT "Isolation and expression of the Interleukin-2 gene from the killer
whale, Orcinus orca.";
RL Mar. Mamm. Sci. 14:531-543(1998).
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.

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CC EMBL; AF009570; AAD01426.1; -
DR HSP; P01585; 1IRL.
DR InterPro; IPR000779; Interleukin-2.
DR Pfam; PF00715; IL2; 1.
DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR PROSITE; PS00424; INTERLEUKIN_2; 1.
DR Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
DR T-cell.

DR	EMBL; L06009; AAA20134.1; -;	1	20	BY SIMILARITY.
DR	EMBL; X69393; CAA49190.1; -;	21	149	INTERLEUKIN-2.
DR	PIR; S31391; S31391.	78	121	BY SIMILARITY.
DR	HSP; P01585; 3INK.	23	23	O-LINKED (GALNAC. .) (BY SIMILARITY)
DR	InterPro; IPR000779; Interleukin-2.	106	106	N-LINKED (GLCNAC. .) (POTENTIAL).
DR	Pfam; PF00715; IL2; 1.	3	3	R -> K (IN REF. 2).
DR	PRINTS; PR00365; INTERLEUKIN2.			
DR	ProDom; PD003649; Interleukin-2; 1.			
DR	SMART; SM00189; IL2; 1.			
DR	PROSITE; PS00424; INTERLEUKIN 2; 1.			
DR	Cytokine; Glycoprotein; Immune response; Signal; Growth factor;			
KW	T-cell.	1	20	BY SIMILARITY.
KW	SIGNAL.	21	149	INTERLEUKIN-2.
FT	CHAIN	78	121	BY SIMILARITY.
FT	DISULFID	23	23	O-LINKED (GALNAC. .) (BY SIMILARITY)
FT	CARBOHYD	106	106	N-LINKED (GLCNAC. .) (POTENTIAL).
FT	CARBOHYD	3	3	R -> K (IN REF. 2).
FT	CONFLICT			

ENBL; M12791; AAA30586.1; -	ALT_INIT.
ENBL; M13204; AAA21143.1; -	
ENBL; X17201; CAA35062.1; -	
ENBL; X52687; CAA36912.1; -	
HSP; P01585; 3INK.	
InterPro; IPR000779; Interleukin-2.	
Pfam; PF00715; I12; 1.	

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DR PRINTS; PR00265; INTERLEUKIN2.
DR ProDom; PD003649; Interleukin-2; 1.
DR SMART; SM00189; IL2; 1.
DR ProSITE; PS00424; INTERLEUKIN-2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.
KW SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 155 INTERLEUKIN-2.
FT DISULFID 79 127 BY SIMILARITY.
FT CARBOHYD 23 23 O-LINKED (GALNAc... ) (BY SIMILARITY).
FT CONFLICT 66 66 V -> A (IN REF. 2).
SQ SEQUENCE 155 AA; 17627 MW; 816667DFEA052EDF CRC64;

Query Match 45.6%; Score 72; DB 1; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.001;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKQLMILNGINN 31
  ||||| 1 : : : ||| : : : 1
Db 21 APTSSSTGNTMKVKSLLLDLQLLEKVKV 50

RESULT 15
IL2_CAPHI
ID IL2_CAPHI STANDARD; PRT; 155 AA.
AC P36835; P79156;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Interleukin-2 precursor (IL-2) (T-cell growth factor) (TCGF).
GN IL2.
OS Capra hircus (Goat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Capra.
OX NCBI_TaxID=9925;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RA Rimstad E.;
RL Submitted (NOV-1993) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Beyer J.C., Cheevers W.P.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: PRODUCED BY T-CELLS IN RESPONSE TO ANTIGENIC OR
CC MITOGENIC STIMULATION, THIS PROTEIN IS REQUIRED FOR T-CELL
CC PROLIFERATION AND OTHER ACTIVITIES CRUCIAL TO REGULATION OF THE
CC IMMUNE RESPONSE. CAN STIMULATE B CELLS, MONOCYTES, LYMPHOKINE-
CC ACTIVATED KILLER CELLS, NATURAL KILLER CELLS, AND GLIOMA CELLS.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: BELONGS TO THE IL-2 FAMILY.
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CC -----
CC EMBL; X76063; CAA53664.1; -.
CC EMBL; U34274; AAB38527.1; -.
CC PIR; S38662; S38662.
CC HSP; P01585; 3INK.
CC InterPro; IPR000779; Interleukin-2.
CC Pfam; PF00715; IL2; 1.
CC PRINTS; PR00265; INTERLEUKIN2.
CC ProDom; PD003649; Interleukin-2; 1.
CC SMART; SM00189; IL2; 1.
CC PROSITE; PS00424; INTERLEUKIN-2; 1.
KW Cytokine; Glycoprotein; Immune response; Signal; Growth factor;
KW T-cell.

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FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 155 INTERLEUKIN-2.
FT DISULFID 79 127 O-LINKED (GALNAc... ) (BY SIMILARITY).
FT CONFLICT 3 5 RMQ -> QTP (IN REF. 2).
FT CONFLICT 22 22 P -> T (IN REF. 2).
FT CONFLICT 30 30 T -> P (IN REF. 2).
FT CONFLICT 51 51 L -> P (IN REF. 2).
FT CONFLICT 71 71 D -> A (IN REF. 2).
FT CONFLICT 89 89 D -> E (IN REF. 2).
FT CONFLICT 99 99 R -> L (IN REF. 2).
FT CONFLICT 107 113 YMASLKG -> SMDNIKR (IN REF. 2).
FT CONFLICT 140 140 Q -> L (IN REF. 2).
FT CONFLICT 144 144 T -> I (IN REF. 2).
FT CONFLICT 154 154 L -> M (IN REF. 2).
SQ SEQUENCE 155 AA; 17703 MW; 90022DFB6AF78DE CRC64;

Query Match 45.6%; Score 72; DB 1; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.001;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKQLMILNGINN 31
  ||||| 1 : : : ||| : : : 1
Db 21 APTSSSTGNTMKVKSLLLDLQLLEKVKV 50

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Search completed: November 22, 2002, 13:11:47
Job time : 11 secs

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GenCore version 5.1.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 13:11:19 : Search time 15 Seconds
(without alignments)
205.087 Million cell updates/sec

Title: US-09-776-781-6

Perfect score: 158

Sequence: 1 MAPSSSTKKTQLQLHLLKLQMLINGINNY 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

PIR 73: *
1: pir1: *
2: pir2: *
3: pir3: *
4: pir4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	147	93.0	153	1 ICHU2	interleukin-2 prec
2	147	93.0	153	1 ICG12	interleukin-2 prec
3	107	67.7	154	2 JN0698	interleukin-2 prec
4	97	61.4	155	2 A31278	interleukin-2 prec
5	96	60.8	154	2 S16241	interleukin-2 prec
6	95	60.1	155	2 S33509	interleukin-2 - mo
7	85	53.8	149	2 S31391	interleukin-2 prec
8	72	45.6	155	2 S38662	interleukin-2 - go
9	72	45.6	155	2 S11488	interleukin-2 prec
10	72	45.6	155	2 I45913	interleukin-2 prec
11	69	43.7	169	2 S37289	interleukin-2 prec
12	64	40.5	169	1 ICWS2	interleukin-2 prec
13	61	38.6	189	2 H64307	hypothetical prote
14	54	34.2	1061	1 GNLJG4	HIV-1 retropepsin
15	53	33.5	357	2 S12169	isopenicillin N ac
16	53	33.5	452	2 B84483	hypothetical prote
17	52.5	33.2	60	2 I68470	interleukin 2 - we
18	51.5	32.6	62	2 I54512	interleukin 2 - mo
19	51.5	32.6	415	2 I51637	cyclin A2 - Africa
20	51	32.3	737	2 G82262	probable exopolysa
21	51	32.3	866	2 F64625	type I restriction
22	51	32.3	875	2 B71890	type I restriction
23	50.5	32.0	72	2 I68871	interleukin 2 - mo
24	50.5	32.0	741	2 A45771	2-5A-dependent RNA
25	50	31.6	304	2 F95285	probable LysR-type
26	50	31.6	543	2 F82217	methyl-accepting c
27	49.5	31.3	367	2 E84453	probable GDSL-moti
28	49.5	31.3	474	2 S31712	beta-1,3-glucanase
29	49	31.0	145	2 H83921	transcription regu

30	48.5	30.7	288	2 B89930	hypothetical prote
31	48.5	30.7	452	2 G64679	anthranilate isome
32	48	30.4	398	2 B70209	conserved hypothet
33	48	30.4	441	2 AB1367	aminopeptidase C I
34	48	30.4	441	2 AC1736	hypothetical prote
35	48	30.4	765	2 S76795	hypothetical prote
36	48	30.4	1964	2 A59282	nonmuscle myosin I
37	47.5	30.1	127	1 NR80K2	pancreatic-type ri
38	47.5	30.1	244	2 T11685	hypothetical prote
39	47	29.7	257	2 S39521	hypothetical prote
40	47	29.7	307	2 T46103	hypothetical prote
41	47	29.7	406	2 S24788	cyclin A - bovine
42	47	29.7	432	2 S08277	cyclin A - human
43	47	29.7	511	2 D71687	alkaline proteinas
44	47	29.7	531	2 T33319	hypothetical prote
45	47	29.7	564	2 S76672	hypothetical prote

ALIGNMENTS

RESULT 1

ICHU2

Interleukin-2 precursor [validated] - human
N:Alternate names: IL-2; T-cell growth factor
C:Species: Homo sapiens (man)
C:Date: 11-Aug-1983 #sequence_revision 11-Aug-1983 #text_change 08-Dec-2000
C:Accession: A01849; A21192; A20961; S31209; A93297; A90113; A93478; I56518; I73624;
R:Holbrook, N.J.; Lieber, M.; Crabtree, G.R.
Nucleic Acids Res. 12, 5005-5013, 1984
A:Title: DNA sequence of the 5' flanking region of the human interleukin 2 gene: homo
A:Reference number: A93524; MUID:84247353; PMID:6330695
A:Accession: A01849
A:Molecule type: DNA
A:Residues: 1-153 <HOL>
A:Cross-references: GB:X00695; GB:X00200; GB:X00201; GB:X00202; NID:g33783; PIDN:CAA2
R:Fujita, T.; Takaoka, C.; Matsui, H.; Taniguchi, T.
Proc. Natl. Acad. Sci. U.S.A. 80, 7437-7441, 1983
A:Title: Structure of the human interleukin 2 gene.
A:Reference number: A21192; MUID:84170243; PMID:6324170
A:Accession: A21192
A:Molecule type: DNA
A:Residues: 1-153 <FUI>
A:Cross-references: GB:J00264; NID:gl86294; PIDN:AAD48509.1; PID:g5729676
R:Holbrook, N.J.; Smith, K.A.; Fornace Jr., A.J.; Comeau, C.M.; Wiskocil, R.L.; Crabt
Proc. Natl. Acad. Sci. U.S.A. 81, 1634-1638, 1984
A:Title: T-cell growth factor: complete nucleotide sequence and organization of the g
A:Reference number: A20961; MUID:84170356; PMID:6608729
A:Accession: A20961
A:Molecule type: DNA
A:Residues: 1-153 <HO2>
A:Cross-references: GB:K02056; NID:gl86302; PIDN:AAA98792.1; PID:g386819
R:Laabi, Y.; Gras, M.P.; Carbone, F.; Brouet, J.C.; Berger, R.; Larsen, C.J.; Tsapi
EMBO J. 11, 3897-3904, 1992
A:Title: A new gene, BCM, on chromosome 16 is fused to the interleukin 2 gene by a t(
A:Reference number: S31208; MUID:93010984; PMID:1396583
A:Accession: S31209
A:Molecule type: mRNA
A:Residues: 11-117 <LAA>
A:Cross-references: EMBL:Z14955
A:Note: this sequence is shown from the beginning of the fragment to the chromosomal
R:Taniguchi, T.; Matsui, H.; Fujita, T.; Takaoka, C.; Kashima, N.; Yoshimoto, R.; Ham
Nature 302, 305-310, 1983
A:Title: Structure and expression of a cloned cDNA for human interleukin-2.
A:Reference number: A93297; MUID:83167472; PMID:6403867
A:Accession: A93297
A:Molecule type: mRNA
A:Residues: 1-153 <TAN>
A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
A:Experimental source: Leukemic T-cell line, Jurkat-111, cloned from Jurkat-FHCRC
R:Maeda, S.; Nishino, N.; Obaru, K.; Mita, S.; Nomiyama, H.; Shimada, K.; Fujimoto, K
Biochem. Biophys. Res. Commun. 115, 1040-1047, 1983
A:Title: Cloning of interleukin 2 mRNAs from human tonsils.

A:Reference number: A90113; MUID:84023840; PMID:6312994
A:Accession: A90113
A:Molecule type: mRNA
A:Residues: 1-153 <MAE>
A:Cross-references: GB:J00264; NID:g186294; PIDN:AA48509.1; PID:g5729676
A:Experimental source: tonsillar mononuclear cells
R:Devos, R.; Plactinck, G.; Cheroutre, H.; Simons, G.; Degraeve, W.; Tavernier, J.; Remau
Nucleic Acids Res. 11, 4307-4323, 1983
A:Title: Molecular cloning of human interleukin 2 cDNA and its expression in Escherichia
A:Reference number: A93478; MUID:83246551; PMID:6306584
A:Accession: A93478
A:Molecule type: mRNA
A:Residues: 1-153 <DEV>
A:Cross-references: GB:V00564; NID:g33780; PIDN:CAA23827.1; PID:g33781
A:Experimental source: splenocytes
R:Elzenberg, O.; Faber-Elman, A.; Lotan, M.; Schwartz, M.
J. Neurochem. 64, 1928-1936, 1995
A:Title: Interleukin-2 transcripts in human and rodent brains: possible expression by as
A:Reference number: I56518; MUID:95239150; PMID:7722480
A:Accession: I56518
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-152 <EIZ>
A:Cross-references: GB:S77834; NID:g999000
A:Accession: I73624
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 5-7,'F',9-17,'P',19-32,'X',34-45,'X',47-143 <RES>
A:Cross-references: GB:S77835; NID:g999001; PIDN:AA414264.1; PID:g4261964
R:Nishino, N.; Obaru, K.; Maeda, S.; Shimada, K.; Onoue, K.
Biomed. Res. 6, 197-205, 1985
A:Title: Organization of the DNA regions flanking the human interleukin 2 gene.
A:Reference number: I52528
A:Accession: I52528
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-68 <REZ>
A:Cross-references: GB:M33199; NID:g186296; PIDN:AA59139.1; PID:g553508
R:Siebenlist, U.; Durand, D.B.; Bressler, P.; Holbrook, N.J.; Norris, C.A.; Kamoun, M.;
Mol. Cell. Biol. 6, 3042-3049, 1986
A:Title: Promoter region of interleukin-2 gene undergoes chromatin structure changes and
A:Reference number: I57603; MUID:87064618; PMID:3491296
A:Accession: I57603
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-68 <RE3>
A:Cross-references: GB:M13879; NID:g186305; PIDN:AA59141.1; PID:g553509
R:Weir, M.P.; Chaplin, M.A.; Wallace, D.M.; Dykes, C.W.; Hobden, A.N.
Biochemistry 27, 6883-6892, 1988
A:Title: Structure-activity relationships of recombinant human interleukin 2.
A:Reference number: I52401; MUID:89062420; PMID:3264184
A:Contents: recombinant IL-2 and mutants expressed in E. coli
A:Accession: I52401
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 'M',21-153 <RE4>
A:Cross-references: GB:M22005; NID:g186300; PIDN:AA59140.1; PID:g386818
A:Note: mutation of Phe-42 to Ala reduced binding to the IL-2 receptor 5-10 fold without
R:Robb, R.J.; Kutny, R.M.; Panico, M.; Morris, H.R.; Chowdhry, V.
Proc. Natl. Acad. Sci. U.S.A. 81, 6486-6490, 1984
A:Title: Amino acid sequence and post-translational modification of human interleukin 2.
A:Reference number: A94009; MUID:85038540; PMID:6333684
A:Accession: A94009
A:Molecule type: protein
A:Residues: 21-153 <ROB>
A:Note: disulfide bonds and carbohydrate binding site were determined
A:Note: heterogeneity in Jurkat-derived IL-2 is primarily due to differences in glycosyl
n in lacking 21-Ala (FT-IL2-A and FT-IL2-B) and 22-Pro (FT-IL2-B)
R:Conradt, H.S.; Nimtz, M.; Dittmar, K.E.J.; Lindenmaier, W.; Hoppe, J.; Hauser, H.
J. Biol. Chem. 264, 17368-17373, 1989
A:Title: Expression of human interleukin-2 in recombinant baby hamster kidney, Ltk-, and
de.
A:Reference number: A34463; MUID:90008901; PMID:2793860

A:Accession: A34463
A:Molecule type: protein
A:Residues: 21-35 <CON>
A:Note: the O-linked glycosylation site in recombinant material matched that from hum
R:Grafenhorst, E.; Hofer, B.; Nimtz, M.; Jaeger, V.; Conradt, H.S.
Eur. J. Biochem. 215, 189-197, 1993
A:Title: Biosynthesis and secretion of human interleukin 2 glycoproteins variants fro
A:Reference number: S34052; MUID:93345493; PMID:8344280
A:Contents: annotation; glycosylation of variant forms expressed in insect cells
C:Genetics:
A:Gene: GDB:IL2
A:Cross-references: GDB:119344; OMIM:147680
A:Map position: 4q26-4q27
A:Introns: 49/3; 69/3; 117/3
C:Superfamily: Interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-153/Product: interleukin-2 #status experimental <IL2>
F:23/Binding site: carbohydrate (Thr) (covalent) #status experimental
F:78-125/Disulfide bonds: #status experimental
Query Match 93.0%; Score 147; DB 1; Length 153;
Best Local Similarity 96.8%; Pred. No. 7.4e-14;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 APTSSSTKKTQLEHLLKLQMLNGINNY 32
Db 21 APTSSSTKKTQLEHLLKLQMLNGINNY 51
RESULT 2
ICG12
Interleukin-2 precursor - common gibbon
N:Alternate names: IL-2; T-cell growth factor
C:Species: Hylobates lar (common gibbon, white-handed gibbon)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 22-Jun-1999
C:Accession: A94067; A01849
R:Chen, S.J.; Holbrook, N.J.; Mitchell, K.F.; Vallone, C.A.; Greengard, J.S.; Crabtre
Proc. Natl. Acad. Sci. U.S.A. 82, 7284-7288, 1985
A:Title: A viral long terminal repeat in the interleukin 2 gene of a cell line that c
A:Reference number: A94067; MUID:86042650; PMID:3877307
A:Accession: A94067
A:Molecule type: mRNA
A:Residues: 1-153 <CHE>
A:Cross-references: GB:M11144; NID:g177014; PIDN:AAA35454.1; PID:g177015
A:Experimental source: leukemia cell line M1A 144; ATCC TIB 201
A:Note: the integration of a retrovirus sequence containing a 5' LTR into the 3' nonc
C:Superfamily: Interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-ce
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-153/Product: interleukin-2 #status predicted <IL2>
F:23/Binding site: carbohydrate (Thr) (covalent) #status predicted
F:78-125/Disulfide bonds: #status predicted
Query Match 93.0%; Score 147; DB 1; Length 153;
Best Local Similarity 96.8%; Pred. No. 7.4e-14;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 2 APTSSSTKKTQLEHLLKLQMLNGINNY 32
Db 21 APTSSSTKKTQLEHLLKLQMLNGINNY 51
RESULT 3
JN0698
Interleukin 2 precursor - cat
C:Species: Felis silvestris catus (domestic cat)
C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 16-Jul-1999
C:Accession: JN0698
R:Cozzi, P.J.; Padrid, P.A.; Takeda, J.; Alegre, M.L.; Yuhki, N.; Leff, A.R.
Biochem. Biophys. Res. Commun. 194, 1038-1043, 1993
A:Title: Sequence and functional characterization of feline interleukin 2.
A:Reference number: JN0698; MUID:93356765; PMID:8352761

A:Accession: JN0698
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-154 <COZ>
A:Cross-references: GB:L19402; NID:g304313; PIDN:AAA02865.1; PID:g304314
C:Superfamily: interleukin-2
C:Keywords: growth factor

Query Match 67.7%; Score 107; DB 2; Length 154;
Best Local Similarity 70.0%; Pred. No. 4.5e-08;
Matches 21; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLHLKLQMLINGINN 31
||||| :||| ||| :||| :||| :|||
Db 21 APASSSTRETQOQLLELLDLKLLGVNN 50

RESULT 4
A31278
interleukin-2 precursor - rat
N:Alternate names: IL-2; T-cell growth factor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 26-Apr-1989 #sequence_revision 26-Apr-1989 #text_change 16-Jul-1999
C:Accession: A45882; A31278
R:McKnight, A.J.; Mason, D.W.; Barclay, A.N.
Immunogenetics 30, 145-147, 1989
A:Title: Sequence of rat interleukin 2 and anomalous binding of a mouse interleukin 2 cDNA
A:Reference number: A45882; MUID:89339608; PMID:2788130
A:Accession: A45882
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <MCK>
A:Cross-references: GB:M22899; NID:g204909; PIDN:AAA41427.1; PID:g204910
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell

Query Match 61.4%; Score 97; DB 2; Length 155;
Best Local Similarity 64.5%; Pred. No. 1.3e-06;
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLHLKLQMLINGINN 32
||||| :||| ||| :||| :||| :|||
Db 21 APTSSPAKETQOHLLELLDLQVLLRGIDNY 51

RESULT 5
S16241
interleukin-2 precursor - pig
N:Alternate names: IL-2; T-cell growth factor
C:Species: Sus scrofa domestica (domestic pig)
C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C:Accession: S16241; S15473
R:Goodall, J.C.; Emery, D.C.; Bailey, M.; English, L.S.; Hall, L.
Biochim. Biophys. Acta 1089, 257-258, 1991
A:Title: cDNA cloning of porcine interleukin 2 by polymerase chain reaction.
A:Reference number: S16241; MUID:91274360; PMID:2054386
A:Accession: S16241
A:Molecule type: mRNA
A:Residues: 1-154 <GOO>
A:Cross-references: EMBL:X56750; NID:g1991; PIDN:CAA40071.1; PID:g1992
R:Lefevre, F.
submitted to the EMBL Data Library, March 1991
A:Description: Molecular cloning of porcine interleukin 2 cDNA by the polymerase chain reaction
A:Reference number: S15473
A:Accession: S15473
A:Molecule type: mRNA
A:Residues: 1-154 <LEF>
A:Cross-references: EMBL:X58428; NID:g2068; PIDN:CAA41330.1; PID:g2069
C:Superfamily: interleukin-2
C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; T-cell
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-154/Product: interleukin-2 #status predicted <MAT>

A:Accession: JN0698
A:Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-154 <COZ>
A:Cross-references: GB:L19402; NID:g304313; PIDN:AAA02865.1; PID:g304314
C:Superfamily: interleukin-2
C:Keywords: growth factor

Query Match 60.8%; Score 96; DB 2; Length 154;
Best Local Similarity 64.5%; Pred. No. 1.7e-06;
Matches 20; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLHLKLQMLINGINN 32
||||| :||| ||| :||| :||| :|||
Db 21 APTSSSTKKTQLEPLLLDLQLLKEVKNY 51

RESULT 6
S33509
interleukin-2 - Mongolian jird
C:Species: Meriones unguiculatus (Mongolian jird)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C:Accession: S33509
R:Mai, Z.; Klei, T.; Horohov, D.
submitted to the EMBL Data Library, October 1992
A:Description: Cross-species PCR cloning of Jird (Meriones unguiculatus) interleukin-2
A:Reference number: S33509
A:Accession: S33509
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-155 <MAI>
A:Cross-references: EMBL:X68779; NID:g577588; PIDN:CAA48679.1; PID:g311638
C:Superfamily: interleukin-2

Query Match 60.1%; Score 95; DB 2; Length 155;
Best Local Similarity 64.5%; Pred. No. 2.5e-06;
Matches 20; Conservative 2; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLHLKLQMLINGINN 32
||||| :||| ||| :||| :||| :|||
Db 21 APTSSPAKEAQOYLEQLLELLDLQQLLRGINNY 51

RESULT 7
S31391
interleukin-2 precursor - horse
C:Species: Equus caballus (domestic horse)
C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999
C:Accession: S31391
R:Tavernor, A.S.; Butcher, G.W.
submitted to the EMBL Data Library, November 1992
A:Description: cDNA cloning of equine interleukin-2 by polymerase chain reaction.
A:Reference number: S31391
A:Accession: S31391
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-149 <TAV>
A:Cross-references: EMBL:X69393; NID:g1076; PIDN:CAA49190.1; PID:g1077
C:Superfamily: interleukin-2

Query Match 53.8%; Score 85; DB 2; Length 149;
Best Local Similarity 53.3%; Pred. No. 6.5e-05;
Matches 16; Conservative 8; Mismatches 6; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLHLKLQMLINGINN 31
||||| :||| ||| :||| :||| :|||
Db 21 APTSSSKRETQOQLQOLQMDLKLLEGVNN 50

RESULT 8
S38662
interleukin-2 - goat
C:Species: Capra aegagrus hircus (domestic goat)
C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 16-Jul-1999
C:Accession: S38662
R:Rimstad, E.
submitted to the EMBL Data Library, November 1993
A:Description: The molecular cloning and expression of caprine interleukin 2.
A:Reference number: S38662
A:Accession: S38662
A:Status: preliminary

A:Molecule type: mRNA
A:Residues: 1-155 <RTM>
A:CROSS-references: EMBL:X76063; NID:g416002; PIDN:CAA53664.1; PID:g416003
C:Superfamily: Interleukin-2

Query Match 45.6%; Score 72; DB 2; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0052;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLNGINN 31
||||||| | : : : ||| | : |
Db 21 APTSSSTGNTMKVKSLDLLQLLEKVKV 50

RESULT 9

S11488

Interleukin-2 precursor - sheep

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C>Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 16-Jul-1999

C:Accession: S11488; S13102; S15317

R:Goodall, J.C.; Emery, D.C.; Perry, A.C.F.; English, L.S.; Hall, L.

Nucleic Acids Res. 18, 5883, 1990

A:Title: cDNA cloning of ovine interleukin 2 by PCR.

A:Reference number: S11488; MUID:91016933; PMID:2216781

A:Accession: S11488

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-155 <GOO>

A:CROSS-references: EMBL:X53934; NID:g1281; PIDN:CAA37881.1; PID:g1282

R:Seow, H.F.; Rothel, J.S.; Radford, A.J.; Wood, P.R.

Nucleic Acids Res. 18, 7175, 1990

A:Title: The molecular cloning of ovine interleukin 2 gene by the polymerase chain reaction

A:Reference number: S13102; MUID:91088336; PMID:2263496

A:Accession: S13102

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-5, 'L', 7-155 <SEO>

A:CROSS-references: EMBL:X55641; NID:g1810; PIDN:CAA39165.1; PID:g1811

R:Bujo, R.; Williamson, M.L.; Sargan, D.R.; Hein, W.H.; McConnell, I.

submitted to the EMBL Data Library, April 1991

A:Reference number: S15517

A:Accession: S15517

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 21-153 <BU>

A:CROSS-references: EMBL:X60148

C:Superfamily: interleukin-2

Query Match 45.6%; Score 72; DB 2; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0052;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLNGINN 31
||||||| | : : : ||| | : |
Db 21 APTSSSTGNTMKVKSLDLLQLLEKVKV 50

RESULT 10

I45913

Interleukin-2 precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 16-Aug-1996 #sequence_revision 16-Aug-1996 #text_change 16-Jul-1999

C:Accession: I45913; S21470; S20761

R:Cerretti, D.P.; McKereghan, K.; Larsen, A.; Cantrell, M.A.; Anderson, D.; Gillis, S.;

Proc. Natl. Acad. Sci. U.S.A. 83, 3223-3227, 1986

A:Title: Cloning, sequence, and expression of bovine interleukin 2.

A:Reference number: I45913; MUID:86205869; PMID:3517854

A:Accession: I45913

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-155 <CER>

A:CROSS-references: GB:M12791; NID:g163204; PIDN:AAA30586.1; PID:g163205

R:Anikeeva, N.N.; Vinogradova, T.V.; Votoshin, O.N.

submitted to the EMBL Data Library, December 1989
A:Reference number: S21470
A:Accession: S21470

A:Molecule type: DNA

A:Residues: 1-22 <AN2>

A:CROSS-references: EMBL:X17201; NID:g452; PIDN:CAA35062.1; PID:g453

C:Genetics:

A:Gene: IL-2

C:Superfamily: Interleukin-2

C:Keywords: cytokine; glycoprotein; growth factor; immunoregulation; lymphokine; T-cell

Query Match 45.6%; Score 72; DB 2; Length 155;
Best Local Similarity 50.0%; Pred. No. 0.0052;
Matches 15; Conservative 6; Mismatches 9; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLNGINN 31
||||||| | : : : ||| | : |
Db 21 APTSSSTGNTMKVKSLDLLQLLEKVKV 50

RESULT 11

S37289

Interleukin-2 precursor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 16-Jul-1999

C:Accession: S37289; S27205; S36162; S24936

R:Todd, J.A.

submitted to the EMBL Data Library, April 1993

A:Reference number: S37289

A:Accession: S37289

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-169 <TOD>

A:CROSS-references: EMBL:X73040

R:Matesanz, F.; Alcina, A.; Pellicer, A.

Biochim. Biophys. Acta 1132, 335-336, 1992

A:Title: A new cDNA sequence for the murine interleukin-2 gene.

A:Reference number: S27205; MUID:93041941; PMID:1420317

A:Accession: S27205

A:Molecule type: mRNA

A:Residues: 1-63 <MATE>

A:CROSS-references: EMBL:X66058; NID:g52725; PIDN:CAA46854.1; PID:g52726

R:Ghosh, S.; Palmer, S.M.; Rodrigues, N.R.; Cordell, H.J.; Hearne, C.M.; Cornwall, R.J.

Nature Genet. 4, 404-409, 1993

A:Title: Polygenic control of autoimmune diabetes in nonobese diabetic mice.

A:Reference number: S36162; MUID:94004970; PMID:8401590

A:Accession: S36162

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-50 <GHO>

A:CROSS-references: EMBL:X73040

C:Superfamily: interleukin-2

C:Keywords: cytokine; glycoprotein; growth factor; lymphokine; T-cell

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-63/Product: interleukin-2 #status predicted <MAT>

Query Match 43.7%; Score 69; DB 2; Length 169;
Best Local Similarity 45.9%; Pred. No. 0.015;
Matches 17; Conservative 6; Mismatches 8; Indels 6; Gaps 1;

QY 2 APTSSSTKKTQIQ-----LEHLLKLQMLNGINN 32
:|||||: | | | | : |
Db 29 SPTSSSTAQAQQQQQQHLEQLLDQLLEKVRMENY 65

RESULT 12

ICMS2

Interleukin-2 precursor - mouse

N:Alternate names: IL-2; T-cell growth factor (TCGF)

C:Species: Mus musculus (house mouse)

C>Date: 30-Jun-1987 #sequence_revision 30-Jun-1987 #text_change 21-Jul-2000

C:Accession: A93550; A54490; A94064; I48597; A01850; I84713

R:Fuse, A.; Fujita, T.; Yasumitsu, H.; Kashima, N.; Hasegawa, K.; Taniguchi, T.

```

Best Local Similarity 37.9%; Pred. No. 0.25;
Matches 11; Conservative 10; Mismatches 8; Indels 0; Gaps 0;

QY 4 TSSSTKKTQLQLHLLKLQMLNGINNY 32
    ||| :|| :|| :|| :|| :|| :|| :||
Db 22 SSSSVLETEIVLDEITKLNLISEINNY 50

RESULT 14
GNLJG4
HIV-1 retropepsin (EC 3.4.23.16) - simian immunodeficiency virus (African green monkey
N;Contains: endonuclease [EC 3.1.-.-]); retropepsin [EC 3.4.23.16]; RNA-directed DNA p
C;Species: simian immunodeficiency virus, SIV
C;Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 03-Jun-2002
C;Accession: B30045
R;Fukasawa, M.; Miura, T.; Hasegawa, A.; Morikawa, S.; Tsujimoto, H.; Miki, K.; Kitam
Nature 333, 457-461, 1988
A;Title: Sequence of simian immunodeficiency virus from African green monkey, a new m
A;Reference number: A30045; MUID:88232906; PMID:3374586
A;Accession: B30045
A;Molecule type: DNA
A;Residues: 1-1061 <FUK>
A;Cross-references: EMBL:X07805; NID:g61748; PID:g1335593
C;Comment: Specific enzymatic cleavages may yield mature proteins including protease,
C;Genetics:
A;Gene: pol
C;Superfamily: pol polyprotein
C;Keywords: aspartic proteinase; hydrolase; nucleotidyltransferase; polyprotein; reve
F;111-210/product: retropepsin #status predicted <RTP>
F;134/Active site: Asp (shared with dimeric partner) #status predicted

Query Match 34.2%; Score 54; DB 1; Length 1061;
Best Local Similarity 58.8%; Pred. No. 17;
Matches 10; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 11 TQLQLHLLKLQMLN 27
    |||::|| :|| :||
Db 976 TQLEIQLQTKIQKILN 992

RESULT 15
SL2169
Isopenicillin N acyltransferase (EC 2.3.1.-) - Emericella nidulans
N;Alternate names: acyl coenzyme A-6-aminopenicillanic acid acyltransferase; acyltran
C;Species: Emericella nidulans, Aspergillus nidulans
C;Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 21-Jul-2000
C;Accession: S12169; A36142; S09090
R;Montenegro, E.; Barrado, J.L.; Gutierrez, S.; Diez, B.; Alvarez, E.; Martin, J.F.
Mol. Gen. Genet. 221, 322-330, 1990
A;Title: Cloning, characterization of the acyl-CoA:6-amino penicillanic acid acyltran
A;Reference number: S12169; MUID:90340281; PMID:2166227
A;Accession: S12169
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <ENB>
A;Cross-references: EMBL:X53310; NID:g2378; PIDN:CAA37394.1; PID:g2379
R;Tobin, M.B.; Fleming, M.D.; Skatrud, P.L.; Miller, J.R.
J. Bacteriol. 172, 5908-5914, 1990
A;Title: Molecular characterization of the acyl-coenzyme A:isopenicillin N acyltransf
herichia coli.
A;Reference number: A36142; MUID:91008967; PMID:2120195
A;Accession: A36142
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-357 <GB>
A;Cross-references: GB:M58293; NID:g167999; PIDN:AAA33287.1; PID:g168000
R;Whiteman, P.A.; Abraham, E.P.; Baldwin, J.E.; Fleming, M.D.; Schofield, C.J.; Suthe
FEBS Lett. 262, 342-344, 1990
A;Title: Acyl coenzyme A: 6-aminopenicillanic acid acyltransferase from Penicillium c
A;Reference number: S09089; MUID:90242961; PMID:2110531
A;Accession: S09090
A;Molecule type: protein
A;Residues: 103-122 <WHI>

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C:Genetics:
A;introns: 12/3; 71/1; 121/3
C:Keywords: acyltransferase
Query Match 33.5%; Score 53; DB 2; Length 357;
Best Local Similarity 52.8%; Pred. No. 7.2;
Matches 10; Conservative 5; Mismatches 4; Indels 0; Gaps 0;
QY 8 TTKTQLQLEHLLKLMIL 26
|||||:|:|:|:|:
Db 40 TTKTQAELEQLRELEQVM 58

Search completed: November 22, 2002, 13:13:26
Job time : 16 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 22, 2002, 13:11:55 ; Search time 10 Seconds
(without alignments)
50.117 Million cell updates/sec

Title: US-09-776-781-6

Perfect score: 158
Sequence: 1 MAPSSSTKKTQLEHLLKLQMLINGINNY 32

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 100480 seqs, 15661496 residues

Total number of hits satisfying chosen parameters: 100480

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	149	94.3	381	10	US-09-822-698A-5
2	147	93.0	133	9	US-10-051-657A-1
3	147	93.0	133	10	US-09-766-543-8
4	147	93.0	153	10	US-09-149-721-3
5	147	93.0	153	10	US-09-923-246-111
6	143	90.5	133	10	US-09-766-543-14
7	143	90.5	331	10	US-09-033-525-2
8	57	36.1	43	10	US-09-835-147-11
9	57	36.1	454	10	US-09-835-147-6
10	57	36.1	478	10	US-09-835-147-8
11	57	36.1	487	10	US-09-835-147-26
12	51	32.3	751	10	US-09-881-752A-280
13	51	32.3	866	10	US-09-815-242-11373
14	50	31.6	37	9	US-10-142-120-1
15	47	29.7	226	10	US-09-796-149-5
16	47	29.7	515	10	US-09-925-300-1285
17	46	29.1	1403	9	US-10-108-605-93
18	44	27.8	284	10	US-09-810-997-1
19	44	27.8	1230	10	US-09-881-752A-150

20	43.5	27.5	84	10	US-09-864-761-36104	Sequence 36104, A
21	43.5	27.5	908	10	US-09-895-072-15	Sequence 15, Appl
22	43.5	27.5	908	10	US-09-986-552-15	Sequence 15, Appl
23	43.5	27.5	928	10	US-09-895-072-1	Sequence 1, Appli
24	43.5	27.5	928	10	US-09-986-552-1	Sequence 1, Appli
25	43	27.2	248	10	US-09-848-294-10	Sequence 10, Appl
26	43	27.2	309	10	US-09-788-626-12	Sequence 12, Appl
27	43	27.2	421	10	US-09-841-132-577	Sequence 577, App
28	43	27.2	473	10	US-09-835-147-29	Sequence 29, Appl
29	43	27.2	990	12	US-10-047-676A-7	Sequence 7, Appli
30	43	27.2	1034	10	US-09-815-242-10331	Sequence 10331, A
31	42.5	26.9	1145	9	US-09-866-557A-5	Sequence 5, Appli
32	42	26.6	45	10	US-09-864-761-43127	Sequence 43127, A
33	42	26.6	214	10	US-09-925-300-1589	Sequence 1589, Ap
34	42	26.6	529	10	US-09-815-242-13935	Sequence 13935, A
35	42	26.6	964	10	US-09-841-132-177	Sequence 177, App
36	42	26.6	977	10	US-09-841-132-191	Sequence 191, App
37	42	26.6	1049	10	US-09-815-242-10072	Sequence 10072, A
38	42	26.6	1049	10	US-09-815-242-13719	Sequence 13719, A
39	41.5	26.3	65	10	US-09-784-869-999	Sequence 999, App
40	41.5	26.3	267	10	US-09-815-242-11549	Sequence 11549, A
41	41	25.9	41	10	US-09-815-242-10672	Sequence 10672, A
42	41	25.9	71	10	US-09-864-761-35411	Sequence 35411, A
43	41	25.9	110	10	US-09-815-242-5029	Sequence 5029, Ap
44	41	25.9	172	10	US-09-864-761-40611	Sequence 40611, A
45	41	25.9	338	10	US-09-841-805A-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1

US-09-822-698A-5

; Sequence 5, Application US/09822698A

; Patent No. US20020146750A1

; GENERAL INFORMATION:

; APPLICANT: Hoogenboom, Hendricus R.J.M.

; TITLE OF INVENTION: MUCIN-1 Specific Binding Members and Methods of Use Thereof

; FILE REFERENCE: DYX-015.1 US

; CURRENT APPLICATION NUMBER: US/09/822,698A

; CURRENT FILING DATE: 2001-03-30

; PRIOR APPLICATION NUMBER: US 09/538,913

; PRIOR FILING DATE: 2000-03-30

; NUMBER OF SEQ ID NOS: 112

; SOFTWARE: Microsoft Word

; SEQ ID NO 5

; LENGTH: 381

; TYPE: PRT

; ORGANISM: artificial sequence

; FEATURE:

; OTHER INFORMATION: MUC1-specific Immunocytokine biVPH1-IL-2

US-09-822-698A-5

Query Match 94.3%; Score 149; DB 10; Length 381;

Best Local Similarity 93.8%; Pred. No. 6e-15;

Matches 30; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTQLEHLLKLQMLINGINNY 32

Db 248 LAPSSSTKKTQLEHLLKLQMLINGINNY 279

RESULT 2

US-10-051-657A-1

; Sequence 1, Application US/10051657A

; Patent No. US20020164300A1

; GENERAL INFORMATION:

; APPLICANT: Chan, Sham-Yuen

; APPLICANT: Kelly, Ruth

; TITLE OF INVENTION: Interleukin-2 Mutein Expressed from Mammalian Cells

; FILE REFERENCE: MSB-7257

; CURRENT APPLICATION NUMBER: US/10/051,657A

; CURRENT FILING DATE: 2002-04-29
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-051-657A-1

Query Match 93.0%; Score 147; DB 9; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.4e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLQMLNGINNY 32
|||||
Db 1 APTSSSTKKTQLEHLLDQLQMLNGINNY 31

RESULT 3
US-09-766-543-8
; Sequence 8, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679,002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: human IL-2
US-09-766-543-8

Query Match 93.0%; Score 147; DB 10; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.4e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLQMLNGINNY 32
|||||
Db 1 APTSSSTKKTQLEHLLDQLQMLNGINNY 31

RESULT 4
US-09-149-721-3
; Sequence 3, Application US/09149721
; Patent No. US20020058795A1
; GENERAL INFORMATION:
; APPLICANT: Mumper, Russ; Tagliaferri, Frank
; TITLE OF INVENTION: HYDROPHOBIC GLYCOSYLAMINE DERIVATIVES, COMPOSITIONS, AND METHODS
; FILE REFERENCE: 237/023
; CURRENT APPLICATION NUMBER: US/09/149,721
; CURRENT FILING DATE: 1998-09-08
; PRIOR APPLICATION NUMBER: US 60/058,259
; PRIOR FILING DATE: 1997-09-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Microsoft Word
; SEQ ID NO 3
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Amino acid sequence of human IL-2
US-09-149-721-3

Query Match 93.0%; Score 147; DB 10; Length 153;
Best Local Similarity 96.8%; Pred. No. 4e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLQMLNGINNY 32
|||||
Db 21 APTSSSTKKTQLEHLLDQLQMLNGINNY 51

RESULT 5
US-09-923-246-111
; Sequence 111, Application US/09923246
; Patent No. US20020128446A1
; GENERAL INFORMATION:
; APPLICANT: No. US20020128446A1ak, Julia E.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Foster, Donald C.
; APPLICANT: Holly, Richard D.
; APPLICANT: Gross, Jane A.
; APPLICANT: Johnston, Janet V.
; APPLICANT: Nelson, Andrew J.
; APPLICANT: Dillon, Stacey R.
; APPLICANT: Hammond, Angela K.
; TITLE OF INVENTION: NOVEL CYTOKINE ZALPHALL LIGAND
; FILE REFERENCE: 99-16
; CURRENT APPLICATION NUMBER: US/09/923,246
; CURRENT FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US/09/522,217
; PRIOR FILING DATE: EARLIER FILING DATE: 2000-03-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/123,904
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: US 60/142,013
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-07-01
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 111
; LENGTH: 153
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-923-246-111

Query Match 93.0%; Score 147; DB 10; Length 153;
Best Local Similarity 96.8%; Pred. No. 4e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKQLQMLNGINNY 32
|||||
Db 21 APTSSSTKKTQLEHLLDQLQMLNGINNY 51

RESULT 6
US-09-766-543-14
; Sequence 14, Application US/09766543
; Patent No. US20020041865A1
; GENERAL INFORMATION:
; APPLICANT: Austin, Richard
; APPLICANT: Kwok, Cheuk S.
; APPLICANT: Ring, David B.
; TITLE OF INVENTION: METHODS FOR TREATING TUMORS
; FILE REFERENCE: PP01679,002
; CURRENT APPLICATION NUMBER: US/09/766,543
; CURRENT FILING DATE: 2000-01-19
; PRIOR APPLICATION NUMBER: 60/177,258
; PRIOR FILING DATE: 2000-01-20
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 14
; LENGTH: 133
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: hIL-2
US-09-766-543-14

US-09-766-543-14

Query Match 90.5%; Score 143; DB 10; Length 133;
Best Local Similarity 96.7%; Pred. No. 1.4e-14;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PTSSSTKKTQLEHLLKLQMLNGINNY 32
Db 2 PTSSSTKKTQLEHLLKLQMLNGINNY 31

RESULT 7

US-09-033-525-2
; Sequence 2, Application US/09033525
; Patent No. US2002009374A1
; GENERAL INFORMATION:
; APPLICANT: Yarkoni, Shai
; APPLICANT: Ben-Yehudah, Ahmi
; APPLICANT: Azar, Yehudith
; APPLICANT: Aqelian, Rami
; APPLICANT: Belotstotsky, Ruth
; APPLICANT: Lotberboun-Galski, Haya
; TITLE OF INVENTION: CHIMERIC PROTEINS WITH CELL-TARGETING
; FILE REFERENCE: 9457-009-999
; CURRENT APPLICATION NUMBER: US/09/033,525
; CURRENT FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 331
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-033-525-2

Query Match 90.5%; Score 143; DB 10; Length 331;
Best Local Similarity 96.7%; Pred. No. 4e-14; Length 331;
Matches 29; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PTSSSTKKTQLEHLLKLQMLNGINNY 32
Db 4 PTSSSTKKTQLEHLLKLQMLNGINNY 33

RESULT 8

US-09-835-147-11
; Sequence 11, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion

; OTHER INFORMATION: construct of human CD39
US-09-835-147-11

Query Match 36.1%; Score 57; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQL 13
Db 25 APTSSSTKKTQL 36

RESULT 9

US-09-835-147-6
; Sequence 6, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 454
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-6

Query Match 36.1%; Score 57; DB 10; Length 454;
Best Local Similarity 100.0%; Pred. No. 0.46;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQL 13
Db 1 APTSSSTKKTQL 12

RESULT 10

US-09-835-147-8
; Sequence 8, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpel, Steven D.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; CURRENT FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955

; PRIOR FILING DATE: 1998-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-8

Query Match 36.1%; Score 57; DB 10; Length 478;
Best Local Similarity 100.0%; Pred. No. 0.49;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQL 13
| | | | | | | | | |
DB 25 APTSSSTKKTQL 36

RESULT 11
US-09-835-147-26
; Sequence 26, Application US/09835147
; Patent No. US20020002277A1
; GENERAL INFORMATION:
; APPLICANT: Maliszewski, Charles R.
; APPLICANT: Gayle III, Richard B.
; APPLICANT: Price, Virginia L.
; APPLICANT: Gimpei, Steven B.
; TITLE OF INVENTION: Inhibitors of Platelet Activation and Recruitment
; FILE REFERENCE: 2879-US
; CURRENT APPLICATION NUMBER: US/09/835,147
; PRIOR FILING DATE: 2001-04-13
; PRIOR APPLICATION NUMBER: US 60/104,585
; PRIOR FILING DATE: 1998-10-16
; PRIOR APPLICATION NUMBER: US 60/107,466
; PRIOR FILING DATE: 1998-11-06
; PRIOR APPLICATION NUMBER: US 60/149,010
; PRIOR FILING DATE: 1999-08-13
; PRIOR APPLICATION NUMBER: PCT/US99/22955
; PRIOR FILING DATE: 1999-10-13
; NUMBER OF SEQ ID NOS: 31
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 26
; LENGTH: 487
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Fusion
; OTHER INFORMATION: construct of human CD39
US-09-835-147-26

Query Match 36.1%; Score 57; DB 10; Length 487;
Best Local Similarity 100.0%; Pred. No. 0.5;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQL 13
| | | | | | | | | |
DB 25 APTSSSTKKTQL 36

RESULT 12
US-09-881-752A-280
; Sequence 280, Application US/09881752A
; Patent No. US20020115078A1
; GENERAL INFORMATION:
; APPLICANT: Kleanthous, Harold
; APPLICANT: Al-Garawi, Amal
; APPLICANT: Miller, Charles
; APPLICANT: Tomb, Jean-Francois
; APPLICANT: Oomen, Raymond P.
; TITLE OF INVENTION: Identification of Polynucleotides

; TITLE OF INVENTION: Encoding No. US20020115078A1el Helicobacter Polypeptides in t
; FILE OF INVENTION: Genome
; FILE REFERENCE: 06132/041002
; CURRENT APPLICATION NUMBER: US/09/881,752A
; CURRENT FILING DATE: 2001-08-15
; PRIOR APPLICATION NUMBER: US 08/833,457
; PRIOR FILING DATE: 1997-04-01
; NUMBER OF SEQ ID NOS: 370
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 280
; LENGTH: 751
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-881-752A-280

Query Match 32.3%; Score 51; DB 10; Length 751;
Best Local Similarity 42.9%; Pred. No. 6.7;
Matches 12; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 5 SSSTKKTQLQLEHLLKLQMLNGINNY 32
| | | | | | | | | | | | | | | |
DB 509 SESQKDKFIKFKILKLENILNSPENF 536

RESULT 13
US-09-815-242-11373
; Sequence 11373, Application US/09815242
; Patent No. US20020061569A1
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John D.
; APPLICANT: Carr, Grant J.
; APPLICANT: Yamamoto, Robert T.
; APPLICANT: Xu, H. Howard
; TITLE OF INVENTION: Identification of Essential Genes in
; FILE REFERENCE: ELITRA.011A
; CURRENT APPLICATION NUMBER: US/09/815,242
; CURRENT FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; NUMBER OF SEQ ID NOS: 14110
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11373
; LENGTH: 866
; TYPE: PRT
; ORGANISM: Helicobacter pylori
US-09-815-242-11373

Query Match 32.3%; Score 51; DB 10; Length 866;
Best Local Similarity 42.9%; Pred. No. 7.9;
Matches 12; Conservative 5; Mismatches 11; Indels 0; Gaps 0;

QY 5 SSSTKKTQLQLEHLLKLQMLNGINNY 32
| | | | | | | | | | | | | | | |
DB 624 SESQKDKFIKFKILKLENILNSPENF 651

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RESULT 14
US-10-142-120-1
; Sequence 1, Application US/10142120
; Patent No. US20020164302A1
; GENERAL INFORMATION:
; APPLICANT: Epstein, Alan L.
; TITLE OF INVENTION: VASOPERMABILITY ENHANCING PEPTIDE FRAGMENT OF HUMAN INTERLEUKIN-
; FILE REFERENCE: 1920-325D2-09801297
; CURRENT APPLICATION NUMBER: US/10/142,120
; CURRENT FILING DATE: 2002-05-09
; PRIOR APPLICATION NUMBER: 09/443,061
; PRIOR FILING DATE: 1999-11-18
; PRIOR APPLICATION NUMBER: 08/806,121
; PRIOR FILING DATE: 1996-12-23
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-142-120-1
Query Match 31.6%; Score 50; DB 9; Length 37;
Best Local Similarity 90.0%; Pred. No. 0.26;
Matches 9; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 23 OMILINGINNY 32
DB 1 EMILINGINNY 10

RESULT 15
US-09-796-149-5
; Sequence 5, Application US/09796149
; Patent No. US20020035079A1
; GENERAL INFORMATION:
; APPLICANT: Univ. of Southern California
; TITLE OF INVENTION: Mutated cyclin G1 protein
; FILE REFERENCE: 4-31342A/USC
; CURRENT APPLICATION NUMBER: US/09/796,149
; CURRENT FILING DATE: 2001-02-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-796-149-5
Query Match 29.7%; Score 47; DB 10; Length 226;
Best Local Similarity 60.0%; Pred. No. 6.4;
Matches 9; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 8 TTKTQLQLEHLHLKL 22
DB 82 TRQVLRMEHLVLKV 96

Search completed: November 22, 2002, 13:14:04
Job time : 11 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: November 22, 2002, 13:11:34 ; Search time 14 Seconds
(without alignments)
67.252 Million cell updates/sec

Title: US-09-776-781-6
Perfect score: 158
Sequence: 1 MAPTSSSTKTKQLQLEHLLKLQMLGINNY 32

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Gap: 10.0 , Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/iaa/6B-COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS-COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	152	96.2	96	1	US-08-160-376A-5
2	152	96.2	96	1	US-08-389-487-8
3	152	96.2	134	6	5496924-55
4	147	93.0	50	1	US-08-127-351-13
5	147	93.0	50	1	US-08-480-367B-13
6	147	93.0	50	1	US-08-487-221A-13
7	147	93.0	50	1	US-08-480-370-13
8	147	93.0	88	4	US-08-817-787-15
9	147	93.0	133	1	US-07-800-366-1
10	147	93.0	133	1	US-08-354-456A-5
11	147	93.0	133	1	US-08-225-224-3
12	147	93.0	133	1	US-08-318-193-89
13	147	93.0	133	1	US-08-284-393B-1
14	147	93.0	133	1	US-08-284-393B-2
15	147	93.0	133	1	US-08-284-393B-3
16	147	93.0	133	1	US-08-734-471-1
17	147	93.0	133	3	US-08-722-258-3
18	147	93.0	133	4	US-08-817-787-13
19	147	93.0	133	4	US-09-310-026-1
20	147	93.0	133	5	PCT-US95-04468-3
21	147	93.0	133	5	PCT-US95-08950-1
22	147	93.0	133	5	PCT-US95-08950-2
23	147	93.0	133	5	PCT-US95-08950-3
24	147	93.0	133	6	5210029-1
25	147	93.0	133	6	5256769-1
26	147	93.0	133	6	5464939-2
27	147	93.0	153	3	US-09-012-366-3

28	147	93.0	153	4	US-08-759-628-8	Sequence 8, Appli
29	147	93.0	153	4	US-09-522-217-111	Sequence 111, App
30	147	93.0	153	6	5314995-7	Patent No. 5314995
31	147	93.0	157	4	US-08-818-562-2	Sequence 2, Appli
32	147	93.0	157	4	US-09-628-445-2	Sequence 2, Appli
33	147	93.0	478	3	US-08-155-888-2	Sequence 2, Appli
34	147	93.0	504	1	US-07-932-915-2	Sequence 2, Appli
35	147	93.0	504	5	PCT-US91-05826-2	Sequence 2, Appli
36	145	91.8	31	4	US-09-116-594-2	Sequence 2, Appli
37	144	91.1	251	3	US-08-875-811-59	Sequence 59, Appl
38	144	91.1	254	3	US-08-875-811-61	Sequence 61, Appl
39	143	90.5	133	1	US-08-354-456A-6	Sequence 6, Appli
40	132.5	83.9	127	3	US-08-806-121B-3	Sequence 3, Appli
41	132.5	83.9	127	4	US-09-443-061-3	Sequence 3, Appli
42	100	63.3	141	4	US-08-930-917A-18	Sequence 18, Appl
43	96	60.8	21	4	US-09-570-921-63	Sequence 63, Appl
44	96	60.8	21	4	US-09-570-921-68	Sequence 68, Appl
45	72	45.6	135	2	US-08-383-621-5	Sequence 5, Appli

ALIGNMENTS

RESULT 1
US-08-160-376A-5
; Sequence 5, Application US/08160376A
; Patent No. 5473049
; GENERAL INFORMATION:
; APPLICANT: Obermeier, Ranier
; APPLICANT: Gerl, Martin
; APPLICANT: Ludwig, Jurgen
; APPLICANT: Sabel, Walter
; TITLE OF INVENTION: Process For Obtaining Proinsulin
; TITLE OF INVENTION: Possessing Correctly Linked
; TITLE OF INVENTION: Cystine Bridges
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kenneth A. Genoni, Esq.
; STREET: Rt. 202-206 No. 5473049th/P.O. Box 2500
; CITY: Somerville
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08876-1258
; COMPUTER READABLE FORM:
; MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
; COMPUTER: IBM 386
; OPERATING SYSTEM: WINDOWS 3.1
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/160,376A
; FILING DATE: December 1, 1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: GE P 4240420.7
; FILING DATE: December 2, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Barbara V. Maurer, Esq.
; REGISTRATION NUMBER: 31,287
; REFERENCE/DOCKET NUMBER: HOE 92/F 384
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 231-4079
; TELEFAX: (908) 231-2255
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 96 Amino Acids
; TYPE: Amino Acid (AA)
; TOPOLOGY: not relevant
; US-08-160-376A-5

Query Match 96.2%; Score 152; DB 1; Length 96;
Best Local Similarity 96.9%; Pred. No. 4.1e-16;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

APPLICATION NUMBER: 934,910

RESULT 5

RESULT 5
US-08-480-367B-13

```
; Sequence 13, Application US/08480367B
; Patent No. 5578288
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LOWE, PRICE, LeBLANC & BECKER
; STREET: 99 Canal Center Plaza, Suite 300
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,367B
; FILING DATE: 07-06-95
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 2654-002A
; TELEPHONE: (703) 684-1111
; TELEFAX: (703) 684-1124
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-480-367B-13

Query Match 93.0%; Score 147; DB 1; Length 50;
Best Local Similarity 96.8%; Pred. No. 1.1e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLNGINNY 32
Db 1 APTSSSTKKTQLQLEHLLKLQMLNGINNY 31

RESULT 6
US-08-487-221A-13
; Sequence 13, Application US/08487221A
; Patent No. 5593656
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESS: NEUSTADT, P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,221A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 413-3000
; TELEFAX: (703) 413-2220
; TELEX: 248955 OPAT UR
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 50 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-487-221A-13

Query Match 93.0%; Score 147; DB 1; Length 50;
Best Local Similarity 96.8%; Pred. No. 1.1e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKLQMLNGINNY 32
Db 1 APTSSSTKKTQLQLEHLLKLQMLNGINNY 31

RESULT 7
US-08-480-370-13
; Sequence 13, Application US/08480370
; Patent No. 5609847
; GENERAL INFORMATION:
; APPLICANT: BELINKA JR, BENJAMIN A.
; APPLICANT: COUGHLIN, DANIEL J.
; APPLICANT: ALVAREZ, VERNON L.
; APPLICANT: WOOD, RICHARD
; TITLE OF INVENTION: METAL-BINDING TARGETED POLYPEPTIDE
; NUMBER OF SEQUENCES: 56
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER &
; ADDRESS: NEUSTADT,
; ADDRESS: P.C.
; STREET: 1755 S. Jefferson Davis Highway, Suite 400
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/480,370
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/127,351
; FILING DATE: 28-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Villacorta, Gilberto M.
; REGISTRATION NUMBER: 34,038
; REFERENCE/DOCKET NUMBER: 4980-004-44
; TELECOMMUNICATION INFORMATION:
```

TELEPHONE: (703) 413-3000
TELEFAX: (703) 413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 50 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-480-370-13

Query Match 93.0%; Score 147; DB 1; Length 50;
Best Local Similarity 96.8%; Pred. No. 1.1e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDLQMLNGINNY 32
|||||
DB 1 APTSSSTKKTQLEHLLDLQMLNGINNY 31

RESULT 8

US-08-817-787-15
Sequence 15, Application US/08817787
Patent No. 6294353
GENERAL INFORMATION:
APPLICANT: Pack, Peter
APPLICANT: Lupas, Andrei
TITLE OF INVENTION: TARGETED HETERO-ASSOCIATION OF
NUMBER OF INVENTIONS: RECOMBINANT PROTEINS TO MULTI-FUNCTIONAL COMPLEXES
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/817,787
FILING DATE: 23-SEP-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: PCT/EP95/04117
FILING DATE:

PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94 11 6558.1
FILING DATE: 20-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Haley Jr., James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090

INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-817-787-15

Query Match 93.0%; Score 147; DB 4; Length 88;
Best Local Similarity 96.8%; Pred. No. 2.2e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDLQMLNGINNY 32
|||||

DB 3 APTSSSTKKTQLEHLLDLQMLNGINNY 33

RESULT 9

US-07-800-366-1
Sequence 1, Application US/07800366
Patent No. 5250296
GENERAL INFORMATION:
APPLICANT: OOTSU, Koichiro
TITLE OF INVENTION: IMMUNOSTIMULANT AGENT CONTAINING
NUMBER OF INVENTIONS: INTERLEUKIN-2 AND 5'-DEOXY-5-FLUOROURIDINE
CORRESPONDENCE ADDRESS:
ADDRESSEE: DAVID G. CONLIN; DIKE, BRONSTEIN, ROBERTS &
ADDRESSEE: CUSHMAN
STREET: 130 Water Street
CITY: Boston
STATE: Massachusetts
COUNTRY: US
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/800,366
FILING DATE: 19911127
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Castle, Donald R
REGISTRATION NUMBER: 24,220
REFERENCE/DOCKET NUMBER: 41417(281)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)523-3400
TELEFAX: (617)523-6440
TELEX: 200291 STRE UR

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-800-366-1

Query Match 93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLDLQMLNGINNY 32
|||||

DB 1 APTSSSTKKTQLEHLLDLQMLNGINNY 31

RESULT 10

US-08-354-456A-5
Sequence 5, Application US/08354456A
Patent No. 5567611
GENERAL INFORMATION:
APPLICANT: Ralph, Peter
APPLICANT: Martin, George
APPLICANT: Platek, Michael
APPLICANT: Larrick, James W.
TITLE OF INVENTION: Multifunctional M-CSF Proteins and Genes Encoding
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: CHIRON CORPORATION
STREET: Intellectual Property - R440, P.O. Box 8097
CITY: Emeryville
STATE: California
COUNTRY: U.S.A.
ZIP: 94662-8097

Query Match 93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;


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; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..133
; OTHER INFORMATION: /label= IL2
US-08-225-224-3

Query Match          93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps

QY      2 APTSSSTKKTKQLQHLLHLLKLQMILGINNY 32
|||||
Db       1 APTSSSTKKTKQLQHLLHLLDLQMILGINNY 31
|||||

RESULT 12
US-08-318-193-89
; Sequence 89, Application US/08318193
; Patent No. 5641663
; GENERAL INFORMATION:
; APPLICANT: GARVIN, Robert T.
; APPLICANT: MALEK, Lawrence T.
; TITLE OF INVENTION: AN EXPRESSION SYSTEM FOR THE SECRETION
; TITLE OF INVENTION: OF BIOACTIVE HUMAN GRANULOCYTE MACROPHAGE COLONY
; TITLE OF INVENTION: STIMULATING FACTOR (GM-CSF) AND OTHER HETEROLOGOUS
; TITLE OF INVENTION: PROTEINS FROM STREPTOMYCES
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 1800 Diagonal Road, Suite 500
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/318,193
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/935,314
; FILING DATE:
; APPLICATION NUMBER: US 07/224,568
; ATTORNEY/AGENT INFORMATION:
; NAME: BENT, Stephen A.
; REGISTRATION NUMBER: 29,768
; REFERENCE/DOCKET NUMBER: 18740/116 CACO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)836-9300
; TELEFAX: (703)683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 89:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-318-193-89

Query Match          93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps

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QY 2 APTSSSTKKTQLEHLLKLQMLNGINNY 32
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Db 1 APTSSSTKKTQLEHLLKLQMLNGINNY 31

RESULT 13
US-08-284-393B-1
; Sequence 1, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-284-393B-1

Query Match 93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLNGINNY 32
    |||||
Db 1 APTSSSTKKTQLEHLLKLQMLNGINNY 31

RESULT 14
US-08-284-393B-2
; Sequence 2, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-284-393B-2

Query Match 93.0%; Score 147; DB 1; Length 133;
Best Local Similarity 96.8%; Pred. No. 3.6e-15;
Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLEHLLKLQMLNGINNY 32
    |||||
Db 1 APTSSSTKKTQLEHLLKLQMLNGINNY 31

RESULT 15
US-08-284-393B-3
; Sequence 3, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 133 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-284-393B-3
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Query Match 93.0%; Score 147; DB 1; Length 133;
 Best Local Similarity 96.8%; Pred. No. 3.6e-15;
 Matches 30; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 APTSSSTKKTQLQLEHLLKQLMILGINNY 32
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 Db 1 APTSSSTKKTQLQLEHLLKQLMILGINNY 31

Search completed: November 22, 2002, 13:13:47
 Job time : 15 secs

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Gapop 10.0 , Gapext 0.5
Searched: 908470 seqs, 13250620 residues
Total number of hits satisfying chosen parameters: 908470
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES			
Result No.	Score	Query Match Length DB ID	Description
1	158	100.0	32 23 ABB79534 Interleukin-2 pept
2	154	97.5	134 8 AAP70573 Sequence of segmen
3	153	96.8	31 23 ABB79535 Interleukin-2 pept
4	153	96.8	133 21 AAY53825 Amino acid sequenc
5	152	96.2	58 12 AAR11015 Human interleukin-
6	152	96.2	60 11 AAR06838 Human IL-2 N-termi
7	152	96.2	60 15 AAR48245 Human Interleukin-
8	152	96.2	96 15 AAR68899 Human pro-insulin
9	152	96.2	96 16 AAR78662 Fusion protein con
10	152	96.2	133 13 AAR22595 Interleukin-2 used

11	152	96.2	134	5	AAP40050	Sequence of an int
12	152	96.2	134	6	AAP50053	Sequence I of new
13	152	96.2	134	6	AAP50855	Sequence encoded b
14	152	96.2	134	7	AAP61102	Sequence of mature
15	152	96.2	134	8	AAP70585	Sequence of human
16	152	96.2	134	11	AAR05267	Sequence of natura
17	152	96.2	134	11	AAR05266	Sequence of natura
18	152	96.2	134	11	AAR05240	Sequence of natura
19	152	96.2	136	20	AAY49917	Human interleukin
20	152	96.2	143	15	AAR50932	tabl. Synthetic.
21	152	96.2	149	11	AAR07265	Recombinant Interl
22	152	96.2	149	11	AAR07266	Recombinant Interl
23	152	96.2	149	11	AAR07267	Recombinant Interl
24	152	96.2	149	11	AAR07269	Recombinant Interl
25	152	96.2	149	11	AAR07148	Recombinant Interl
26	152	96.2	149	11	AAR07149	Recombinant Interl
27	152	96.2	149	11	AAR07150	Recombinant Interl
28	152	96.2	149	11	AAR07261	Recombinant Interl
29	152	96.2	149	11	AAR07262	Recombinant Interl
30	152	96.2	149	11	AAR07263	Recombinant Interl
31	152	96.2	149	11	AAR07264	Recombinant Interl
32	152	96.2	172	10	AAP94809	Human interleukin
33	152	96.2	201	11	AAR06839	Human IL-2 N-termi
34	152	96.2	255	6	AAP50305	Fused antibody inter
35	152	96.2	273	6	AAP50087	Conjugate of inter
36	152	96.2	273	6	AAP50310	Interferon-gamma a
37	150	94.9	133	21	AAY53829	Amino acid sequenc
38	149	94.3	65	10	AAP91032	Human interleukin-
39	149	94.3	133	21	AAY53828	Amino acid sequenc
40	149	94.3	149	11	AAR07146	Recombinant Interl
41	149	94.3	149	11	AAR07268	Recombinant Interl
42	149	94.3	149	11	AAR07255	Recombinant Interl
43	149	94.3	149	11	AAR07256	Recombinant Interl
44	149	94.3	149	11	AAR07257	Recombinant Interl
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ALIGNMENTS

RESULT 1			
ABB79534			
ID	ABB79534	standard; Peptide; 32 AA.	
XX	ABB79534;		
AC	ABB79534;		
XX			
DT	23-SEP-2002	(first entry)	
XX			
DE	Interleukin-2 peptide IP131	(D20K).	
XX			
KW	IP131; interleukin-2; human; gene; gene therapy; mutant; mutein.		
XX			
OS	Homo sapiens.		
OS	Synthetic.		
XX			
FH	Key	Location/Qualifiers	
FT	Misc-difference 21		
FT	/note= "wild-type Asp substituted by Lys"		
XX			
PN	US2002044935-Al.		
XX			
PD	18-APR-2002.		
XX			
PF	06-FEB-2001; 2001US-0776781.		
XX			
PR	16-JUL-1998; 98US-0116594.		
PR	12-SEP-2000; 2000US-0660465.		
XX			
PA	(INSP) INST PASTEUR.		
XX			
PI	Theze J, Eckenberg R, Moreau J, Goldberg M, Rose T, Alzari P;		
PI	Mazie J;		
XX			

DR WPI: 2002-546505/58.
DR N-PSDB; ABN84295.
XX
PT New peptides derived from Interleukin 2 designated IP130 and IP131 are
PT useful as therapeutic agents in the treatment of patients deficient in
PT IL-2 activity -
XX
PS Claim 18; Page 2; 53pp; English.
XX
CC The present sequence is the protein sequence for IP131 D20K. The
CC sequence is based on the human interleukin-2 (IL-2) peptide IP130
CC (see ABN84292) by the addition of a C-terminal Tyr residue, and
CC substitution of the native Asp-20 residue by Lys. Asp-20 is
CC located in a region of IL-2 that directly influences interaction of
CC the cytokine with its receptor (IL-2R). An antibody that binds to
CC the peptide is claimed, and is preferably an antibody produced by
CC hybridoma H2-8 (CNCM No. I-2338). A claimed method of detecting
CC the presence or activity of involves contacting a sample with
CC IP131 D20K, and detecting whether binding occurs. A claimed method
CC for inhibiting IL-2R activity involves contacting IL-2R with the
CC peptide. A claimed method for inducing IL-2 activity in a patient
CC comprises administering IP131 D20K to the patient. A vector
CC containing DNA encoding the peptide is claimed, and is used in a
CC claimed method for treating a patient deficient in IL-2 activity.
CC Also claimed are peptides corresponding to IP131 D20K but
CC containing conservative amino acid substitutions, i.e. change of
CC non-polar R-groups but other non-polar R-groups, change of
CC uncharged polar R-groups by other uncharged polar R-groups,
CC substitution of Arg by Lys, Asp by Glu, Thr by Ser, or Asn by
CC Gln, and vice versa. The peptide induces SHC phosphorylation or
CC induction of the SHC/MAPK pathway. Antibodies specific for the
CC peptide are useful for treatment or prevention of undesirable
CC immune reactions such as graft rejection, or autoimmune disorders
CC such as rheumatoid arthritis.
XX
SQ Sequence 32 AA;

Query Match 100.0%; Score 158; DB 23; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTQLQLEHLLKQLMILNGINNY 32
Db 1 MAPSSSTKKTQLQLEHLLKQLMILNGINNY 32

RESULT 2
AAP70573
AC AAP70573 standard; Protein; 134 AA.
XX
XX AAP70573;
XX
DT 27-MAY-1991 (first entry)
XX
DE Sequence of segments A-F of interleukin-2 (IL-2).
XX
KW Interleukin-2 fusion protein; ballast fragment.
XX
PN DE3636903-A.
XX
PD 02-JUL-1987.
XX
XX 30-OCT-1986; 86DE-3636903.
XX
XX 21-DEC-1985; 85DE-3545565.
PR 30-OCT-1986; 86DE-3636903.
XX
PA (FARH) HOECHST AG.
XX
XX Habermann P;
PI
DR WPI: 1987-186353/27.
DR N-PSDB; AAN70921.

XX
PT New fusion protein contg. small interleukin 2 ballast fragments -
PT allowing control of product solubility, and corresp. genes,
XX vectors and transformed host cells
XX
PS Disclosure; pp8-9; 22pp; German.
XX
CC The inventors claim a novel fusion protein which has a C- or N-
CC terminal portion corresponding essentially to the MA sequence of
CC interleukin-2 (IL-2) but contg. less than 100 AAs. The IL-2 sequence
CC is coded for by 1,2 or 3 of the A-F segments of the IL-2 gene having
CC the formula: (EcoRI)-A-PstI-B-MinI-C-XbaI-D-SacI-E-PvuII-F-(SalI),
CC for example, the sequence in AAN70921. The segments are joined in any
CC appropriate sequence and opt. connected by usual adaptors or linkers.
XX
SQ Sequence 134 AA;

Query Match 97.5%; Score 154; DB 8; Length 134;
Best Local Similarity 96.9%; Pred. No. 4.7e-14;
Matches 31; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTQLQLEHLLKQLMILNGINNY 32
Db 1 MAPSSSTKKTQLQLEHLLKQLMILNGINNY 32

RESULT 3
ABB79535
ID ABB79535 standard; Peptide; 31 AA.
XX
XX ABB79535;
AC
XX 23-SEP-2002 (first entry)
DT
XX Interleukin-2 peptide IP131 (D20K).
DE
KW IP131; interleukin-2; human; gene; gene therapy; mutant; mutetin.
XX
XX Homo sapiens.
OS
XX Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 20 /note= "wild-type Asp substituted by Lys"
FT
XX
XX US2002044935-A1.
XX
PD 18-APR-2002.
XX
XX 06-FEB-2001; 2001US-0776781.
XX
PR 16-JUL-1998; 98US-0116594.
PR 12-SEP-2000; 2000US-0660465.
XX
XX (INSP) INST PASTEUR.
PA
XX These J, Eckenberg R, Moreau J, Goldberg M, Rose T, Alzari P;
PI Mazie J;
XX
XX WPI; 2002-546505/58.
DR N-PSDB; ABN84296.
DR
XX New peptides derived from Interleukin 2 designated IP130 and IP131 are
PT useful as therapeutic agents in the treatment of patients deficient in
PT IL-2 activity -
XX
PS Claim 18; Page -; 53pp; English.
XX
CC The present sequence is the protein sequence for IP131 D20K. The
CC sequence is based on the human interleukin-2 (IL-2) peptide IP130
CC (see ABN84292) by the addition of a C-terminal Tyr residue, and
CC substitution of the native Asp-20 residue by Lys. Asp-20 is
CC located in a region of IL-2 that directly influences interaction of
CC the cytokine with its receptor (IL-2R). An antibody that binds to
CC the peptide is claimed, and is preferably an antibody produced by
CC hybridoma H2-8 (CNCM No. I-2338). A claimed method of detecting
CC the presence or activity of involves contacting a sample with
CC IP131 D20K, and detecting whether binding occurs. A claimed method
CC for inhibiting IL-2R activity involves contacting IL-2R with the
CC peptide. A claimed method for inducing IL-2 activity in a patient
CC comprises administering IP131 D20K to the patient. A vector
CC containing DNA encoding the peptide is claimed, and is used in a
CC claimed method for treating a patient deficient in IL-2 activity.
CC Also claimed are peptides corresponding to IP131 D20K but
CC containing conservative amino acid substitutions, i.e. change of
CC non-polar R-groups but other non-polar R-groups, change of
CC uncharged polar R-groups by other uncharged polar R-groups,
CC substitution of Arg by Lys, Asp by Glu, Thr by Ser, or Asn by
CC Gln, and vice versa. The peptide induces SHC phosphorylation or
CC induction of the SHC/MAPK pathway. Antibodies specific for the
CC peptide are useful for treatment or prevention of undesirable
CC immune reactions such as graft rejection, or autoimmune disorders
CC such as rheumatoid arthritis.
XX
SQ Sequence 32 AA;

Query Match 100.0%; Score 158; DB 23; Length 32;
Best Local Similarity 100.0%; Pred. No. 2.7e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAPSSSTKKTQLQLEHLLKQLMILNGINNY 32
Db 1 MAPSSSTKKTQLQLEHLLKQLMILNGINNY 32

RESULT 2
AAP70573
AC AAP70573 standard; Protein; 134 AA.
XX
XX AAP70573;
XX
DT 27-MAY-1991 (first entry)
XX
DE Sequence of segments A-F of interleukin-2 (IL-2).
XX
KW Interleukin-2 fusion protein; ballast fragment.
XX
PN DE3636903-A.
XX
PD 02-JUL-1987.
XX
XX 30-OCT-1986; 86DE-3636903.
XX
XX 21-DEC-1985; 85DE-3545565.
PR 30-OCT-1986; 86DE-3636903.
XX
PA (FARH) HOECHST AG.
XX
XX Habermann P;
PI
DR WPI: 1987-186353/27.
DR N-PSDB; AAN70921.

Sequence 58 AA:

XX OS Homo sapiens.
XX PN FR2692594-A.

XX	24-DEC-1993.	92FR-0007571
PD		
XX		
PF	22-JUN-1992:	

PR 22-JUN-1992; 92FR-000/5/1.
XX
XX (PERE/) PEREZ J.
XX

FI XX
Perez J,

DR WFL, 1994 020230/04.
DR N-PSDB: AAO55629, AAO55630.

PT Application of optimised gene expression - for scientific,

XX
FI Industrial and therapeutic purposes

ES
disclosure, fry 20 and fry 22, topp, french
XX

CC resonances between coding and non-coding regions were measured for
CC the native human IL-2 gene in plasmid pT911 (see AAO55630) and a

PD 02-AUG-1990.

PF 24-JAN-1989; 89JP-0013270.

PR 24-JAN-1989; 89JP-0013270.

PA (AJIN) AJINOMOTO KK.

DR WPT; 1990-278851/

sq	sequence	00 AA,
	Query Match	96.2%; Score 152; DB 15; Length 60;
	Best Local Similarity	96.9%; Pred. No. 3.8e-14;

PS Disclosure; Fig 2; 11pp; Japanese.

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Db	1	MATPSSSKKKTQLOLEHLLDLOMILNGINNY	32

Sequence 60 AA:

XX AAR68899;
AC
XX
DT 02-MAR-1995 (first entry)

AA	
DE	Human pro-insulin 2.
XX	
KW	Pro-insulin; A-chain; B-chain; C-chain; disulphide;
KW	mercaptan; chaotropic agent.

XX	
OS	Homo sapiens.
XX	
PN	EP600372-A

AA AAR48245;

PF 25-NOV-1993; 93EP-0118993.
 XX
 PR 02-DEC-1992; 92DE-4240420.
 XX
 PA (FARH) HOECHST AG.
 XX

PI Gerl M, Ludwig J, Obermeier R, Sabel W;
 XX WPI; 1994-177718/22.
 XX

XX Prodn. of pro-insulin with correct di-sulphide bridges - by
 PT treating recombinant precursor protein with mercaptan in alkali
 PT and in presence of chaotropic agent, then isolation on
 PT hydrophobic resin
 XX

PS Disclosure; Page 11; 15pp; German.

XX Pro-insulin is produced by treating recombinant precursor protein
 CC with a mercaptan to provide 2-10 SH residues per Cys residue, in
 CC presence of a chaotropic agent and in aq. medium of pH 10-11,
 CC treating the prod. with 3-50 g hydrophobic adsorber resin per 1 aq.
 CC medium of pH 4-7, isolating the adsorbed resin and pro-insulin and
 CC desorbing the pro-insulin. This method produces pro-insulin with
 CC correctly bonded Cys bridges. Compared with known methods it
 CC involves fewer stages (esp. no sulphitolysis or cyanogen bromide
 CC cleavage) and overall losses during purification are reduced, i.e.
 CC the process is quicker and gives better yields.
 CC Sequences of insulin chain A, B and C are given in AAR68895-97.
 CC Sequences of pro-insulin 1-4 are given in AAR68898-901.
 XX

SQ Sequence 96 AA;

Query Match 96.2%; Score 152; DB 15; Length 96;
 Best Local Similarity 96.9%; Pred. No. 6.3e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPTSSSTKTKTQLEHLLKQLMILNGINNY 32
 DB 1 MAPTSSSTKTKTQLEHLLKQLMILNGINNY 32

RESULT 9

AAR78662
 ID AAR78662 standard; protein; 96 AA.

AC AAR78662;

DT 03-APR-1996 (first entry)

DE Fusion protein contg. proinsulin sequence 3.

XX Proinsulin; post-translational modification; recombinant production;
 KW protein folding; conformation.

XX Synthetic.

FT Key Location/Qualifiers
 FT Region 41..44
 FT /label= R2
 FT /note= "a peptide of 4 amino acids"
 FT Peptide 45..74
 FT /label= R1-(B2-B29)-Y
 FT /note= "human insulin B-chain"
 FT Region 75
 FT /label= X
 FT Peptide 76..96
 FT /label= Gly-(A2-A20)-R3
 FT /note= "human insulin A-chain"

XX EP68292-A2.

XX 23-AUG-1995.

XX

PF 09-FEB-1995; 95EP-0101748.

XX

PR 18-FEB-1994; 94DE-4405179.

XX

PA (FARH) HOECHST AG.

XX

PI Gerl M, Ludwig J, Obermeier R, Sabel W;

XX WPI; 1995-284754/38.

XX

XX Isolation of insulin that is correctly post-translationally

PT processed - by reacting pro-insulin with a mercaptan in the presence
 PT of a chaotropic agent and purificn. after absorption to hydrophobic
 PT resin
 XX

PS Example 2; Page 8; 16pp; German.

XX The present sequence is that of a fusion protein, produced in E.coli
 CC which contains an example of a proinsulin molecule corresp.
 CC to the general formula R2-R1-(B2-B29)-Y-X-Gly-(A2-A20)-R3 (II). In
 CC formula (II), X = Lys, Arg or a peptide of 2-35 amino acids contg.
 CC Lys or Arg at the N- and C-termini; Y = a natural amino acid; R1 =
 CC Phe or a bond; R2 = H, Arg, Lys, a peptide of 2-45 amino acids
 CC contg. Arg or Lys at the N- and C-termini; R3 = a natural amino
 CC acid; (A2-A20) and (B2-B29) are the insulin A- and B-chain sequences
 CC from human or other insulin. The proinsulin molecule, released by
 CC cyanogen bromide, is reacted with mercaptan at a ratio of 2-10 SH
 CC residues of mercaptan per Cys residue of proinsulin. The reaction
 CC takes place in the presence of a chaotropic auxiliary agent at
 CC pH 10-11 and results in proinsulin with correctly linked cystine
 CC bridges. Reaction with trypsin and opt. carboxypeptidase B yields
 CC correctly folded insulin. The insulin is isolated by absorption on
 CC a hydrophobic resin.
 XX

SQ Sequence 96 AA;

Query Match 96.2%; Score 152; DB 16; Length 96;
 Best Local Similarity 96.9%; Pred. No. 6.3e-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPTSSSTKTKTQLEHLLKQLMILNGINNY 32

DB 1 MAPTSSSTKTKTQLEHLLKQLMILNGINNY 32

RESULT 10

AAR22595

ID AAR22595 standard; Protein; 133 AA.

XX

AC AAR22595;

DT 03-NOV-1992 (first entry)

XX

DE Interleukin-2 used to make hybrid proteins.

XX

KW IL-2; hybrid; diphtheria; toxin; DT; proliferation; peripheral blood;
 KW mononuclear cells; PBMC; auto-immune response; diabetes; rheumatoid;
 XX arthritis; allograft rejection; T-suppressor.

XX Homo sapiens.

OS

XX WO9206117-A.

PN

XX 16-APR-1992.

PD

XX 27-SEP-1991; 91WO-US07342.

PF

XX 28-SEP-1990; 90US-0590113.

PR

XX (SERA-) SERAGEN INC.

PA (UYHO-) UNIVERSITY HOSPITAL.

XX

PI Murphy JR, Svrluga R;

XX WPI; 1992-150820/18.
DR N-PSDB; AAQ23867.
XX
PT Hybrid protein comprising portion of the IL-2 binding domain -
PT useful for inhibiting unwanted immune responses e.g. autoimmune
PT diseases and reaction to organ and tissue transplants
XX
XX Disclosure; Fig 1; 37pp; English.
PS
XX The interleukin-2 protein is part of a hybrid protein comprising
CC the binding domain of IL-2 and an enzymatically inactive fragment
CC of diphtheria toxin which does not include a functional DT
CC generalised eukaryotic binding site (see AAR26486). The hybrid
CC protein is capable of stimulating the proliferation of peripheral
CC blood mononuclear cells in vitro and of suppressing an immune
CC response in a mammal in vivo. The hybrid protein allows the
CC inhibition of an unwanted immune response such as autoimmune disease,
CC e.g. diabetes and rheumatoid arthritis, or allograft rejection. It
CC does not cause general immunosuppression, so avoids the resulting
CC risk of life threatening infections. In the treatment of allograft
CC rejection the hybrid protein spares donor-specific T-suppressor cells,
CC which can thus proliferate and aid in prolonging graft survival. The
CC hybrid protein does not need to be tailored to individual patients but
CC can be used as a universal inhibiting agent. Therapy need not be
CC continuous following allograft or an acute stage of autoimmune
CC disease, but can be discontinued after a course of treatment.
XX
XX Sequence 133 AA;
SQ
Query Match 96.2%; Score 152; DB 13; Length 133;
Best Local Similarity 96.9%; Pred. No. 9e-14;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAPSSSTKTKTQLEHLLKLMILNGINNY 32
Db 1 MAPSSSTKTKTQLEHLLKLMILNGINNY 32
RESULT 11
AAP40050
ID AAP40050 standard; Protein; 134 AA.
XX
AC AAP40050;
XX
DT 14-JAN-1992 (first entry)
XX
DE Sequence of an interleukin-2-like polypeptide encoded by the DNA
DE insert of pSV-hIL2-O or pSV-hIL2-1.
XX
KW Diagnosis; therapy; cancer; tumour-specific cytotoxic cell; AIDS;
KW multiple sclerosis; lupus; rheumatoid arthritis; herpes;
KW viral disease; lymphokine.
XX
XX Homo sapiens.
XX
XX EP118977-A.
XX
PD 19-SEP-1984.
XX
XX 25-JAN-1984; 84EP-0300439.
XX
PR 10-JUN-1983; 83GB-0015981.
PR 08-FEB-1983; 83GB-0003383.
XX
XX (BIOJ) BIOGEN NV.
XX
XX Fiers WC, Devos RR;
PI
XX WPI; 1984-232548/38.
DR N-PSDB; AAN40042.
XX
XX Prodn. of human Interleukin 2-like polypeptide(s) - useful

PT Instead of IL-2 for stimulating the immune system etc.
XX
PS Claim 6; Page 57-58; 69pp; English.
XX
CC The DNA sequence is esp. selected from a human chromosomal gene bank,
CC e.g. it is a hIL-2 related portion of lamda CH4A-ghIL-2-1 or -2, or
CC of lamda L47-ghIL-2-1, -2 or -3. Transformed hosts are also claimed,
CC esp. E.coli, Ps spp., B.subtilis, B.stearothermophilus. IL-2-like
CC polypeptides are also claimed.
XX
XX Sequence 134 AA;
SQ
Query Match 96.2%; Score 152; DB 5; Length 134;
Best Local Similarity 96.9%; Pred. No. 9.1e-14;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MAPSSSTKTKTQLEHLLKLMILNGINNY 32
Db 1 MAPSSSTKTKTQLEHLLKLMILNGINNY 32
RESULT 12
AAP50053
ID AAP50053 standard; Protein; 134 AA.
XX
AC AAP50053;
XX
DT 16-AUG-2002 (updated)
DT 03-SEP-1991 (first entry)
XX
DE Sequence I of new biologically active Interleukin 2 (IL-2).
XX Immunological agent; lymphokine.
XX
OS Homo sapiens.
OS Synthetic.
XX
PN EP163249-A.
XX
PD 04-DEC-1985.
XX
PF 28-MAY-1985; 85EP-0113324.
XX
PR 29-MAY-1984; 84DE-3419995.
XX
PA (FARH) HOECHST AG.
XX
PI Engels J, Uhlmann E, Wengenmayer F, Mullner H, Winnacker EL;
PI Mertz R, Okazaki H;
XX
DR WPI; 1985-304738/49.
DR N-PSDB; AAN50037.
XX
PT New biologically active interleukin 2 fragments and derivs. - and
PT coding DNA sequences, intermediate oligo-nucleotide(s), hybrid
PT plasmid(s) and transformed cells
XX
PS Disclosure; Page 18-20; 33pp; German.
XX
CC DNA SQs coding for AAs 1-133 and 0-133 (an additional Met) of IL-2
CC are claimed, including the CDS of SQ 1 (see AAN50037) with/without 1
CC or 2 stop codons. The use of a synthetic gene is esp. convenient
CC for expression in E. coli and allows modification of the AA SQ to
CC improve peptide stability, solubility or activity. The synthetic
CC gene was made from a series of oligonucleotides ligated to form four
CC larger fragments designated IL 2-I to 2-IV (see AAN50038).
CC (Updated on 16-AUG-2002 to add missing OS field.)
XX
XX Sequence 134 AA;
SQ
Query Match 96.2%; Score 152; DB 6; Length 134;
Best Local Similarity 96.9%; Pred. No. 9.1e-14;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLEHLLKQLQMLINGINNY 32
 DB 1 MAPTSSSTKKTQLEHLLKQLQMLINGINNY 32

RESULT 13

AAP50855
 ID AAP50855 standard; Protein; 134 AA.

XX AC AAP50855;
 XX DT 03-OCT-2002 (updated)
 XX DT 01-DEC-1991 (first entry)

XX DE Sequence encoded by synthetic interleukin II (IL-2) gene.

XX KW Immunotherapy; lymphokine; interleukin-2; thymocyte mitogenesis.

XX OS Synthetic.

XX PN W08500817-A.

XX PD 28-FEB-1985.

XX PF 09-AUG-1984; 84WO-US01252.

XX PR 03-AUG-1984; 84US-0635941.

XX PR 10-AUG-1983; 83US-0521967.

XX PA (AMGE-) AMGEN.

XX PI Souza LM, Stabinsky Y;

XX WPI; 1985-062280/10.

XX DR N-PSDB; AAN50535.

XX PT Microbial expression of interleukin II and analogues - by using
 PT manufactured DNA sequences to transform microorganisms

XX PS Example; Table IV, Page 15-16; 39pp; English.

XX CC The inventors claim a manufactured gene for the prodn. of IL-2 and
 CC analogues, and for polypeptides of IL-2 and analogues, and for
 CC methods for their recombinant production.
 CC (Updated on 03-OCT-2002 to add missing OS field.)

XX SQ Sequence 134 AA;

Query Match 96.2%; Score 152; DB 6; Length 134;
 Best Local Similarity 96.9%; Pred. No. 9.le-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLEHLLKQLQMLINGINNY 32
 DB 1 MAPTSSSTKKTQLEHLLKQLQMLINGINNY 32

RESULT 14

AAP61102
 ID AAP61102 standard; Protein; 134 AA.

XX AC AAP61102;

XX DT 09-MAR-1992 (first entry)

XX DE Sequence of mature human interleukin 2 (IL2) encoded by SUN-IL2.

XX KW Yeast expression vector; lymphokine.

XX OS Homo sapiens.

XX PN EP171000-A.

XX PD 12-FEB-1986.
 XX PF 26-JUL-1985; 85EP-0109405.
 XX PR 27-JUL-1984; 84JP-0157038.
 XX PA (SUNR) SUNTORY LTD.

XX PI Oshima T, Tanaka S, Tsujimoto M, Nakazato H;

XX WPI; 1986-043554/07.

XX DR N-PSDB; AAN60198.

XX PT Protein and peptide prodn. by immobilised yeast transformant -
 PT contg. expression vector which induces secretion of prod. from
 PT cell into culture medium

XX PS Disclosure; Fig 6 and Page 31; 53pp; English.

XX CC The inventors claim a method for the prodn. of a substance having
 CC the AA SQ of AAP61102. The method uses a synthetic DNA SQ (AAN60198). A
 CC composition contg. a protein having human IL2 activity which is
 CC produced by the method is also claimed. The method uses yeast
 CC transformed by a secretory expression vector.

XX SQ Sequence 134 AA;

Query Match 96.2%; Score 152; DB 7; Length 134;
 Best Local Similarity 96.9%; Pred. No. 9.le-14;
 Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLEHLLKQLQMLINGINNY 32

DB 1 MAPTSSSTKKTQLEHLLKQLQMLINGINNY 32

RESULT 15

AAP70585

ID AAP70585 standard; protein; 134 AA.

XX AC AAP70585;

XX DT 10-APR-1991 (first entry)

XX DE Sequence of human interleukin-2 (IL-2).

XX KW Lymphokine.

XX OS Homo sapiens.

XX PN DE3541856-A.

XX PD 04-JUN-1987.

XX PF 27-NOV-1985; 85DE-3541856.

XX PR 27-NOV-1985; 85DE-3541856.

XX PA (FARH) HOECHST AG.

XX PI Habermann P, Mengenmayer F;

XX DR WPI; 1987-157830/23.

XX DR N-PSDB; AAN70931.

XX PT Fusion proteins contg. interleukin 2 aminoacid sequences - as
 PT well as genes coding for these proteins, vectors contg. the
 PT genes, and host cells contg. the vectors

XX PS Example; pp 7-8; 20pp; German.

XX CC Prefd. fusion proteins are of formula Met-X-Y-Z or Met-Z-Y-X. Where

CC X-an AA sequence corresp. essentially to approx. the first 100 AAs
CC of human interleukin-2; Y-a direct bond or bridge of genetically
CC codable AAs which facilitates the cleaving off of the AA sequence Z;
CC Z-a sequence of genetically codable AAs.
XX

SQ Sequence 134 AA;

Query Match 96.2%; Score 152; DB 8; Length 134;
Best Local Similarity 96.9%; Pred. NO. 9.1e-14;
Matches 31; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MAPTSSSTKKTQLQLEHLLKQLQMLNGINNY 32

Db 1 MAPTSSSTKKTQLQLEHLLKQLQMLNGINNY 32

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